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Title:
Perfect score:
Sequence:
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No.
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Maximum
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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DB
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66.5
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seq length: 2000000000
     of hits satisfying chosen parameters:
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Match
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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*
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    AGEDALRPWKSTAKHPWFQI.....LQGDVIWLRCVPELRVDYTS
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    729
676
672
693
1938
1938
240
2340
3310
790
7746
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7746
7789
7789
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             US-08-947-965-71
US-09-252-991A-32535
US-08-947-965-76
US-09-514-302-2
US-09-514-302-2
US-09-152-060-100
US-09-152-060-64
US-09-152-060-64
US-09-960-780-4
US-08-960-780-4
US-08-968-373-14
US-08-968-373-14
US-08-968-373-14
US-08-968-373-14
US-09-328-352-8096
US-09-328-352-8096
US-09-328-352-8096
US-09-33-352A-6
US-09-233-352A-6
US-09-233-352A-6
US-09-233-752A-6
US-09-233-752A-6
US-09-233-752A-6
US-09-233-752A-6
US-09-233-752A-6
US-09-233-752A-6
US-09-233-752A-6
US-09-402-036-6
US-08-471-044-29
US-08-463-483A-29
US-08-463-483A-32
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Sequence 71, Appl
Sequence 76, Appli
Sequence 4, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 27542, A
Sequence 64, Appli
Sequence 6, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 14, Appli
Sequence 14, Appli
Sequence 6, Appli
Sequence 32, Appl
                                                                                                                                                                                                                                                                                                                                                                       Description
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RESULT 2 US-09-252-991A-32535 ; Sequence 32535, Application US/09252991A ; Patent No. 6551795 ; GENERAL INFORMATION: ; APPLICANT: Marc J. Rubenfield et al. ; APPLICANT: Marc J. Rubenfield et al. ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCE	Qy 12 TAKHPWFQIEDNRCYIDNGKLFARGSIVGNMSRFVFDFKADYGGVGENL	NS-08-947-965-71 Query Match Best Local Similarity Matches 25; Conser	EARLIER NUMBER SOFTWAR SEQ ID N LENGTH TYPE: ORGANI	NATION NUMBER: 04 DATE: 1995-04-2 ATION NUMBER: 11 DATE: 1995-10-1 ATION NUMBER: 12 ATION NUMBER: 12 DATE: 1995-11-1 DATE: 1995-11-1	TITLE OF INVENTION: Variants FILE REFERENCE: 4285.204-US CURRENT APPLICATION NUMBER: US/08/ CURRENT FILING DATE: 1997-10-09	ESULT 1 IS-08-947-965-71 Sequence 71, Applicat Patent No. 6004790 GENERAL INFORMATION: Dijkhuize APPLICANT: Dijkstra, AppLICANT: Andersen, AppLICANT: Osten, Cl TITLE OF INVENTION:	ALIGNMENTS	2 789 2 US-08-469-334-32 2 789 3 US-09-300-529-29 2 789 3 US-09-300-529-32 2 789 3 US-09-233-336A-2 2 789 3 US-09-233-752A-2 2 789 3 US-09-233-752A-2 2 789 3 US-09-233-752A-4 2 789 3 US-09-233-752A-4 2 789 3 US-09-402-036-2 2 789 4 US-09-402-036-4 2 789 4 US-09-002-285-92 2 789 4 US-09-002-285-92	8 64 10.2 789 2 US-08-471-046A-32 9 64 10.2 789 2 US-08-470-566B-29 0 64 10.2 789 2 US-08-470-566B-32 1 64 10.2 789 2 US-08-838-219B-2 2 64 10.2 789 2 US-08-838-219B-4 2 64 10.2 789 2 US-08-838-219B-4 3 64 10.2 789 2 US-08-469-334-29
es relating to pseudo	YGGVGENLYVHADDVEFVP 71	h 676; ls 13; Gaps 3;		·				8 2 4 2 4 C 4 C 8 8 C C C C C C C C C C C C C C	224232

Rubenfield et al.
NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

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CURRENT APPLICATION NUMBER: US/08/947,965A
CURRENT FILING DATE: 1997-10-09
EARLIER APPLICATION NUMBER: 0477/95
EARLIER FILING DATE: 1995-04-21
EARLIER FILING DATE: 1995-04-21
EARLIER APPLICATION NUMBER: 1173/95
EARLIER FILING DATE: 1995-10-17
EARLIER APPLICATION NUMBER: 1281/95
EARLIER FILING DATE: 1995-11-16
EARLIER APPLICATION NUMBER: PCT/DK96/00179
EARLIER APPLICATION NUMBER: PCT/DK96/00179
EARLIER FILING DATE: 1996-04-22
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 76
LENGTH: 675
TYPE: PRT
ORGANISM: Bacillus obbensis
RESULT 4
US-09-514-302-4
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PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 32535
LENGTH: 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Dijkhuizen, Lubbert
APPLICANT: Dijkstra, Bauke
APPLICANT: Andersen, Carsten
APPLICANT: Osten, Claus von der
TITLE OF INVENTION: Cyclomaltodextrin Glucanotransferase
TITLE OF INVENTION: Variants
FILE REFERENCE: 4285.204-US
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Best Local Similarity 29.3
Matches 34; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
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                                                                                                                                                                                                                                                                                            Local
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                                                                                                                                  72 GE-SIKWNVRNIDVMPIFETLALRIVLQGDVIWI-RCVPELRVD 113
                                                                                                                                                                                                                       12 TAKHPWFQIEDNRCYIDNGKLFARGSIVGNMSRFVFDPKADYGGVGENLYVHADDVEFVP 71
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                                                                                                                                                                                                                                                                    l Similarity
26; Conserv
                                                                                           YEDSIYRNLYDLADYDLNNTVMDQYLKESIKLWLDKGIDGIRVD 222
                                                                                                                                                                             TPNHSSPALETDPSYAENGAVYNDGVLIGNYSN---DP-----NNLFHHNGGTDFSS 178
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BER: US_60/074,788
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29.3%; Pred. No. 2.3;
ative 16; Mismatches
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25.0%; Pred. No. 4.8;
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                                                                                                                                                                                                                   ; TYPE: PRT; ORGANISM: Bacillus US-09-514-302-2
                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: GENE FOR ENZYME HAVING BO
TITLE OF INVENTION: ALKALINE ALPHA-AMYLASE AC
FILE REFERENCE: 2173-105P
CURRENT APPLICATION NUMBER: US/09/514,302
CURRENT FILING DATE: 2000-02-28
EARLIER APPLICATION NUMBER: 08/952,084
EARLIER FILING DATE: 1997-11-10
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 2
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Best Local Similarity 32.0%;
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                                                                                                                                          Matches
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Best Local
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APPLICANT: IGARASHI,
APPLICANT: OZAKI, Ka
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CURRENT FILING DATE: 2000-02-28
EARLIER APPLICATION NUMBER: 08/952,084
EARLIER FILING DATE: 1997-11-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: GENE FOR ENZYME HAVING TITLE OF INVENTION: ALKALINE ALPHA-AMYLASE FILE REFERENCE: 2173-105P
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APPLICANT: ITO, Susumu
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SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: OZAKI, KATSUYA
APPLICANT: ARA, Katsutoshi
APPLICANT: KAWAI, Shuji
APPLICANT: ITO, Susumu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: HATADA,
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tent No. 6338959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 893
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                                                         1127 SVKSGWKLIDEMYAY--DGKLGAELHEDGTATLKVWSPKADNVSVVLYDKVDQNEVV--D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 TAKHPWFQIEDNRCYIDNGKLFARGSIVGNMSRFVFDPKAD-----YGGVGENLYVHAD 65
66 DVEFVPGESLKWNVR 80 : | | |: |:
                                                                                           12 TAKHPWFQIEDNRCYIDNGKLFARGSIVGNMSRFVFDPKAD-----YGGVGENLYVHAD 65
                                                                                                                                          24;
                                                                                                                                                             Similarity
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                                                                                                                                                                                  Length 1938;
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US-09-152-060-100
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              SUPINITH: 240
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Patent No. 6551795
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                                                                                                EARLIER APPLICATION NUMBER: 60/068,368 EARLIER FILING DATE: 1997-12-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                        EARLIER APPLICATION NUMBER: PCT/US98/04858
EARLIER FILING DATE: 1998-03-12
EARLIER APPLICATION NUMBER: 60/040,762
EARLIER FILING DATE: 1997-03-14
                                                            SOFTWARE: PatentIn Ver.
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                                                                                 NUMBER OF SEQ
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TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPLICANT: Marc J. Rubenfield et al.

ITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

ITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LE REFERENCE: PZ003P1.US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TLE OF INVENTION: 28 Human Secreted Proteins
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                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/040,710 FILING DATE: 1997-03-14 APPLICATION NUMBER: 60/050,934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/152,060 FILING DATE: 1998-09-11
                                                                                                                                                                                                      APPLICATION NUMBER: 60/048,189
FILING DATE: 1997-05-30
APPLICATION NUMBER: 60/057,765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100, Application US/09152060
                                                                                                                                              APPLICATION NUMBER: 60/048,970 FILING DATE: 1997-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27 IDNGKLFARGSIVGNMSRFVFDPKADY-----GGVGENLYVHADDVEFVPGESLK--WN 78
                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/048,357 FILING DATE: 1997-05-30
                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/048,100
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                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                      FILING DATE: 1997-09-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h 10.9%; Score 68.5; DI Similarity 28.9%; Pred. No. 7.9;
                                                                                                                                                                                                                                                                                                                                                      LING DATE: 1997-05-30
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; ORGANISM: Homo sapiens US-09-152-060-100
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US-09-152-060-64
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                                                                                                                                      Matches
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NAME/KEY: SITE
LOCATION: (297)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EARLIER APPLICATION NUMBER: PCT/US98/04858 EARLIER FILING DATE: 1998-03-12
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                                                                                                                                                                                                                                                                                                            NAME/KEY: SITE
LOCATION: (35)
                                                                                                                                                                                                                          OTHER INFORMATION: Xaa equals any of the naturally occurring
                                                                                                                                                                                                                                                                                               OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                 EATURE:
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                                                                  151 RHAVYQAEHLLQTAGTCGVSDDSL---GSLLGPRTAAVFRPRP-----GDSLPSRETRYV 202
203 ELYVVVDNAEFOMLGSEAAVRHRVLEVVNHVDKLYQKLNFRVVLVGLEIW 252
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                                                                                                    14 KHPWFQIED-----NRCYIDNGKLFARGSIVGNMSRFVFDPKADYGGVGEN----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37 RHAVYQAEHLLQTAGTCGVSDDSL---GSLLGPRTAAVFRPRP-----GDSLPSRETRYV
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                                                                                                                                     Similarity
29; Conserv
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                            -LYVHADDVEF-VPGESLKWNVRNLDVM----PIFETLALRLVLQGDVIW 103
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26.4%; Pred. No. 5;
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Pred. No. 3.
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Patent No. 64/2---
Patent No. 64/2---
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SCHULZ, GEORG E.
APPLICANT: CANDUSSIO, ANTON
APPLICANT: WICH, GUNTER
TITLE OF INVENTION: CYCLODEXTRIN
FILLE OF INVENTION: CYCLODEXTRIN
FILLE REFERENCE: SCHULZ-W2 CIP
CURRENT APPLICATION NUMBER: US/09/430,702
CURRENT FILING DATE: 1999-10-29
CURRENT APPLICATION NUMBER: 08/816,317

TTER APPLICATION NUMBER: 08/816,317
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US-09-430-702-1
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                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09430702 Patent No. 6472192
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Best Local Similarity
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LENGTH: 391 amin
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:

NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REGISTRATION NUMBER: 34,090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151 RHAVYQAEHLLQTAGTCGVSDDSL---GSLLGPRTAAVFRPRP-----GDSLPSRETRYV 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 -LYVHADDVEF-VPGESLKWNVRNLDVM----PIFETLALRLVLQGDVIW 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.7%; Score 67; DB 3; Length 391; 26.4%; Pred. No. 6.2;
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                                            US-08-960-780-4
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GENERAL II
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
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Best Local Similarity
Matches 15; Conserv
Query Match
Best Local Similarity
                                                                                                                                                                                     TELEFAX: 352-372-5800 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PI
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ORGANISM: Bacillus sp. 1-1
                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/960,780
                                                          MOLECULE TYPE: protein ORIGINAL SOURCE: 36a
                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                               FILING DATE: 30-OCT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: No. 6204435el Pesticidal Toxins and Nucleotide
                                                                                                                       TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: MA-708
                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 30-OCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Gainesville
                                                                                                                                                                                                                    TELEPHONE:
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                                                                                                           TOPOLOGY:
                                                                                                                                                        LENGTH:
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                                                                                                                                                       790 amino acids
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Dullum, Charles Joseph
Muller-Cohn, Judy
Stamp, Lisa
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                                                                                                           linear
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10.5%;
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25.9%; Pred. No. 1.1;
cive 10; Mismatches
                                                                                                                                                                                                                                                                                                                                US 60/029,848
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Pred.
 No.
 DB 3;
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US-09-073-898-4
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                                                                                                       TELEFAX: 352-372-5800
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 790 amino acids
                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 60/
FILING DATE: 30-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 30-OCT-1997
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                               REFERENCE/DOCKET NUMBER: MA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                  NAME: Sanders, Jay M. REGISTRATION NUMBER:
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                                                                 TOPOLOGY:
                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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                                                                                             amino acid
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2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Finstad-Lee, Stacey
VENTION: No. 6242669el Pesticidal Toxins and Nucleotide
VENTION: Sequences Which Encode These Toxins
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                                                              linear
                                              protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            George
                                                                                                                                                                                                                                                                                                  US 08/960,780
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                                                                                                                                                                                                                                39,355
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; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-08-868-373-14
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US-09-328-352-8096
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                                                                                                                 SEQ ID NO 8096
LENGTH: 587
TYPE: PRT
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Best Local S
Matches 32
 Query Match
Best Local S
Matches 21
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APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                            Sequence 8096, Application US/09328352
Patent No. 6562958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local Similarity
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                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
                                                                                                                                                                                                                                  FILE REFERENCE: GTC99-03PA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: FATTY ACID ELONGASES FILE REFERENCE: 07148/064001 CURRENT APPLICATION NUMBER: US/08/868,373 CURRENT FILING DATE: 1997-06-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Jaworski, Jan G.
APPLICANT: Post-Beittenmiller, Martha A.
APPLICANT: Todd, James
                                                                                             ORGANISM: Acinetobacter baumannii
 Local Similarity 23.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           336 RCVYQEQDDTGRTGVSL---SKDLMAIAGETLKTNITTLGPLVLPISEQILFFMTLVVKK 392
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10.3%; Score 65; DB 4; Length 587; 23.9%; Pred. No. 19; ative 21; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.4%; Score 65.5; D
31.8%; Pred. No. 14;
Live 12; Mismatches
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PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 17381
LENGTH: 310
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17381
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US-09-252-991A-17381
; Sequence 17381, Application US/09252991A
; Patent No. 6551795
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Search completed: January 22, 2004, 11:38:42 Job time: 22.7747 secs
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: AUCCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                     Query Match 10.3%; Score 64.5; DB 4; Length 310; Best Local Similarity 23.2%; Pred. No. 9.2; Matches 29; Indels 45; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 107196.136
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              193 QQKPD 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      294 QİBALSENRVHLQTSRRFABGALIĞQVARFIQMQTSQIDHEQVLQQFEIDIVQVSELRSI 353
                                                                                                                                              109 ELRVD 113
                                                                                                                                                                                              138 TEVYPGVVDTLKWLKRNGVEMALITNKPERFVAPILDEMKLGRYFRWIIGGDTL-----P 192
                                                                                                                                                                                                                                      67 VEFVPG--ESLKWNVRN------LDVMPIFETLAL----RLVLQGDVIWLRCVP 108
                                                                                                                                                                                                                                                                                        87 İEKVRQWIGNGARVLVRRALAĞSI-----EHDĞIĞEEETEAALALFMEAYADSHAL 137
                                                                                                                                                                                                                                                                                                                                  20 IEDNRCYIDNG-KLFARGSIVGNMSRFVFDPKADYGGVGEN-----LYVHADD--- 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QIE---DNRCYIDNGKLFARGSIVGNMSRFV--FDPKADYGGVGENL---YVHADDVEFV 70
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                       7654021
                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                Score
           91
75.5
69
69
67.5
67.5
67.5
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seq length: 2000000000
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*

12: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

15: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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Match
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Gapop 10.0 ,
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14.5
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           199
186
301
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WS-10-300-393-20
WS-10-369-493-2939
WS-10-014-436-4
WS-10-014-436-2
WS-10-369-493-7954
WS-10-375-932-89
WS-10-375-932-89
WS-10-375-932-89
WS-10-375-932-89
US-10-375-932-89
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     Sequence 19, Appl Sequence 20, Appl Sequence 2939, Ap Sequence 4, Appli Sequence 7954, Ap Sequence 25, Appli Sequence 25, Appl Sequence 89, Appl Sequence 585, Appl Sequence 100, App Sequence 100, App Sequence 100, App Sequence 100, App Sequence 64, Appl Sequence 64, Appl Sequence 64, Appl Sequence 64, Appl Sequence 64, Appl
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ALIGNMENTS

บร-10-300-393-19

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RESULT 2
US-10-300-393-20
; Sequence 20, Application US/10300393
; Publication No. US20030118568A1
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; TYPE: PRT
; ORGANISM: human cytomegalovirus Towne strain
US-10-300-393-19
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Publication No. US20030118568A1

GENERAL INFORMATION:
APPLICANT: Crew, Mark D.
TITLE OF INVENTION: Viral Stealth Technology to Prevent T-Cell-Mediated Rejection
TITLE OF INVENTION: Xenografts
FILE REFERENCE: 8793-50391
CURRENT APPLICATION NUMBER: US/10/300,393
CURRENT FILING DATE: 2002-11-19
PRIOR APPLICATION NUMBER: US 60/342,981
PRIOR APPLICATION NUMBER: US 60/342,981
PRIOR APPLICATION NUMBER: US 60/342,981
PRIOR FILING DATE: 2001-12-18 ---
NUMBER OF SEQ ID NOS: 22
                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 629; DB 15; Best Local Similarity 100.0%; Pred. No. 2.6e-68; Matches 116; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                            199;
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GENERAL INFORMATION:

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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 2939
LENGTH: 301
TYPE: PRT
ORGANISM: Thermotoga maritima
US-10-369-493-2939
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; TYPE: PRT
; ORGANISM: human cytomegalovirus Towne strain US3
US-10-300-393-20
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                                                                       US-10-014-436-4
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Sequence 4, Application US/10014436 Publication No. US20020182699A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: POSEQ ID NO 20
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                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 8793-50391
CURRENT APPLICATION NUMBER: US/10/300,393
CURRENT FILING DATE: 2002-11-19
PRIOR APPLICATION NUMBER: US 60/342,981
PRIOR FILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 22
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TITLE OF INVENTION: Viral Stealth Technology to Prevent T-Cell-Mediated Rejection
TITLE OF INVENTION: Xenografts
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                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                      263 -APEELIKDLLKNWNVSNIVIRKPNLEDVFLKL 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37 FRVEENQCWSHMGMLHYKGRMSGNFTEKHFVSVGIVSQSYMDRLQVSGEQYHHDE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 FQIEDNRCYIDNGKLFARGSIVGNMSR-----FVFDPKADYGGVGENLYVHADDVEFV 70
                                                                                                                                                                                                                                                                                                              19 QIEDNRCYIDNGKLFARG-----SIVGNMSRFVFDPKAD----YGGVGENLYVHADDVE 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71 PGESLKWNV-----RNLDVMPIFETLALRLVLQGD-VIWLRCVPELRVDYTS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31; Conservative
                                                                                                                                                                                                                                                                                                                                                           30; Conservative
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                                                                                                                                                                                                               FVPGESLK-----WNVRNLDV-MPIFETLALRL 95
                                                                                                                                                                                                                                                                                                                                                                                 12.0%; Score 75.5; DB 32.3%; Pred. No. 0.96;
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27.4%; Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                           11; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                        DB 12; Length 301;
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                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                            ; LENGTH: 1938
; TYPE: PRT
; ORGANISM: Bacillus
US-10-014-436-2
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                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: JP 111547/1995
PRIOR FILING DATE: 1995-05-10
PRIOR APPLICATION NUMBER: PCT/JP96/01243
PRIOR FILING DATE: 1996-05-10
PRIOR APPLICATION NUMBER: US 08/952,084
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: US 09/514,302
PRIOR FILING DATE: 2000-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 11.0%;
Best Local Similarity 32.0%;
Matches 24; Conservative 1:
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                                                                                                                                                    SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/10014436 Publication No. US20020182699A1
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Gene for Enzyme Having Both Alkaline Pullulanase and Alkaline Alph TITLE OF INVENTION: Amylase Activites
FILE REPERENCE: 2173-0122P
CURRENT APPLICATION NUMBER: US/10/014,436
CURRENT FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: DF 111547/1995
PRIOR APPLICATION NUMBER: DFT/JP96/01243
PRIOR APPLICATION NUMBER: PCT/JP96/01243
PRIOR FILING DATE: 1996-05-10
PRIOR APPLICATION NUMBER: US 08/952,084
PRIOR APPLICATION NUMBER: US 08/952,084
PRIOR APPLICATION NUMBER: US 08/952,084
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: US 09/514,302
PRIOR FILING DATE: 2000-02-28
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                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Gene for Enzyme Having TITLE OF INVENTION: Amylase Activites FILE REFERENCE: 2173-0122P CURRENT APPLICATION NUMBER: US/10/014,436 CURRENT FILING DATE: 2002-05-21
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                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: KAWAI, Shuji
APPLICANT: ITO, Susumu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: HATADA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82 SVKSGWKLIDEMYAY--DGKLGAELHEDGTATLKVWSPKADNVSVVLYDKVDQNEVV--D 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 TAKHPWFQIEDNRCYIDNGKLFARGSIVGNMSRFVFDPKAD-----YGGVGENLYVHAD 65
                                                                                                                                                                       PatentIn version 3.1
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OZAKI, Katsuya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IGARASHI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Katsutoshi
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11.0%;
32.0%;
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 Score
Pred.
 No.
 DB 14;
59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Both Alkaline Pullulanase and Alkaline Alph
                      Length 1938;
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25.0%;

Pred. No. 15;

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US-10-375-932-25
; Sequence 25, Application US/10375932
; Publication No. US20040009469A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 7954
LENGTH: 384
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                                                                                                             NUMBER OF SEQ ID NOS: 345
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 25
LENGTH: 448
TYPE: PRT
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Best Local Similarity
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Query Match
                                                                                                                                                                                                      APPLICANT: Punnonen, Juha
APPLICANT: Brinkman, Alice M.
APPLICANT: Brinkman, Alice M.
FILE REFERENCE: 0322.210US
CURRENT APPLICATION NUMBER: US/10/375,932
CURRENT FILING DATE: 2003-02-26
PRIOR APPLICATION NUMBER: US 60/360,030
PRIOR FILING DATE: 2002-02-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10(52052)B CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
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                                                        OTHER INFORMATION: Synthetic polypeptide: 16B4-NPRM
                                                                        ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66 DVEFVPGESLKWNVR 80
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Slater, Steven C.
Goldman, Barry S.
Chen, Xianfeng
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10.7%; Score 67.5;
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 DB 12;
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 Length 448;
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US-10-375-932-89
; Sequence 89, Application US/10375932
; Publication No. US20040009469A1
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                                                    NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 585
LENGTH: 564
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ORGANISM: Deinococcus radiodurans
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                                                                                                               FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/375,932
CURRENT FILING DATE: 2003-02-26
PRIOR APPLICATION NUMBER: US 60/360,030
PRIOR FILING DATE: 2002-02-26
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APPLICANT: Punnonen, Juha
APPLICANT: Brinkman, Alice M.
APPLICANT: Brinkman, Alice M.
TITLE OF INVENTION: NOVEL FLAVIVIRUS ANTIGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 345
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                                                                                                                                                                                                             TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10(52052)B
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Synthetic polypeptide:
                                                                                                                                                                                                                                                                                                                                                                                                              blication No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       327 GEDA-----PCKIP-FSTEDEKGVTONGRLITANPIVTEKDSPVNIEAEPPFGESYIVV 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 396 GVGDKAL----
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                                                                                                                                                                                                                                                                          Hinkle, Gregory J.
Slater, Steven C.
Goldman, Barry S.
Chen, Xianfeng
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5. US20030233675A1
                                                                                                                                                                                                                                                                                                                                                                   Yongwei
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25.0%; Pred. No. 15;
tive 12; Mismatches
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US-09-853-161-100
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                                                       PRIOR APPLICATION NUMBER: 09/152,060
PRIOR FILING DATE: 1998-09-11
PRIOR APPLICATION NUMBER: PCT/US98/04858
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/040,762
PRIOR PILING DATE: 1997-03-14
PRIOR APPLICATION NUMBER: 60/040,710
PRIOR APPLICATION NUMBER: 60/040,710
PRIOR FILING DATE: 1997-03-14
PRIOR FILING DATE: 1997-03-14
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LENGTH: 6291
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Publication No. US20030198981A1
GENERAL INFORMATION:
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Best Local
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APPLICANT: ZAZOPOULOS, Emmanuel
APPLICANT: STAFFA, Alfredo
TITLE OF INVENTION: GENES AND PROTEINS INVOLVED IN THE BIOSYNTHESIS OF LIPOPEPTIDES
FILE REFERENCE: 3002-11US
                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/853,161
CURRENT FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: 60/265,583
PRIOR FILING DATE: 2001-02-02
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SOFTWARE: PatentIn version 3.0
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CURRENT FILING DATE: 2002-12-24
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TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: PZ003P3
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                   APPLICATION NUMBER: 60/050,934 FILING DATE: 1997-05-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          823 TGTGERMYRTGDLVRRVPGE 842
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          136 PNHTSSDHAWFQ-----EALTGKASAKRDWYVWRDPAPDGGLPNNWKSFFGGPAWTLDE 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56 VGENLYVHADDVEFVPGE-SLKWNVRNLDV-MPIFETLA--LRLVLQG---DVIWLRCVP 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54 GGVGENLYVHADDVEFVPGE 73
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NUMBER: 60/048,100
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 ; ORGANISM: Homo sapiens
US-09-852-659A-100
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SEQ ID NO 100
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LENGTH: 240
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Best Local Similarity
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PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/048,189
PRIOR FILING DATE: 1997-05-30
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PRIOR FILING DATE: 1997-09-05
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PRIOR APPLICATION NUMBER: 09/152,060
PRIOR FILING DATE: 1998-09-11
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FILING DATE: 1997-03-14
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APPLICATION NUMBER: 60/048,970
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APPLICATION NUMBER: 60/057,765
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18; Mismatches
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RESULT 14
US-09-853-161-64
; Sequence 64, Application US/09853161
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TYPE: PRT
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TILE OF INVENTION: 28 Human Secreted Proteins
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RESULT 15
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US-09-853-161-64
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rocal Similarity
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SEQ ID NO 64
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APPLICANT: Rosen et
                                             CURRENT APPLICATION NUMBER: US/09/852,659A
CURRENT FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: 60/265,583
PRIOR FILING DATE: 2001-02-02
                                                                                                                       APPLICANT: Rosen et al. TITLE OF INVENTION: 28 Human Secreted Proteins FILE REFERENCE: PZ003P4
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NAME/KEY: SITE
LOCATION: (35)
OTHER INFORMATION: X
NAME/KEY: SITE
LOCATION: (297)
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CURRENT FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: 60/265,583
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TITLE OF INVENTION: 28 Human Secreted Proteins
              PRIOR APPLICATION NUMBER: 09/152,060 PRIOR FILING DATE: 1998-09-11
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ORGANISM: Homo
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APPLICATION NUMBER: PCT/US98/04858
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Pred. No. 12;
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PRIOR APPLICATION NUMBER: 60/057,765

PRIOR APPLICATION NUMBER: 60/048,970

PRIOR PILING DATE: 1997-09-06

PRIOR APPLICATION NUMBER: 60/068,368

PRIOR APPLICATION NUMBER: 60/068,368

PRIOR PILING DATE: 1997-12-19

NUMBER OF SEQ ID NOS: 121

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 64

LENGTH: 335

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: SITE

LOCATION: (35)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

FEATURE:

NAME/KEY: SITE

LOCATION: (297)

COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

FEATURE:

NAME/KEY: SITE

LOCATION: (297)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-09-852-659A-64
Search completed: January 22, 2004, 12:09:28 Job time : 283.676 secs
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DR APPLICATION NUMBER: 60/040,762
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DR APPLICATION NUMBER: 60/040,710
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DR APPLICATION NUMBER: 60/050,934
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APPLICATION NUMBER: 60/048,189
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                                                                                                            252 ELYVVVDNAEFQMLGSEAAVRHRVLEVVNHVDKLYQKLNFRVVLVGLEIW
                                                                                                                                                                                                                         151 RHAVYQAEHLLQTAGTCGVSDDSL---GSLLGPRTAAVFRPRP-----GDSLPSRETRYV 202
                                                                                                                                            60 -LYVHADDVEF-VPGESLKWNVRNLDVM----PIFETLALRLVLQGDVIW 103
                                                                                                                                                                                                                                                                       14 KHPWFQIED-----NRCYIDNGKLFARGSIVGNMSRFVFDPKADYGGVGEN------
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     AGEDALRPWKSTAKHPWFQI.....LQGDVIWLRCVPELRVDYTS 116
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     GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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HQLF1 precursor -
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QQBEC6
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Result No.

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65.5	65.5	65.5	66	66	66.5	66.5	66.5	66.5	66.5	66.5	67	67	67	67	67
10.4	10.4	10.4	10.5	10.5	10.6	10.6	10.6	10.6	10.6	10.6	10.7	10.7	10.7	10.7	10.7
489	286	273	361	261	1208	1151	463	463	233	159	7463	1690	757	381	367
N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N
G91143	T38680	H81140	JN0716	AI0742	T27822	S48431	AC0964	D41853	E86340	F75021	T36248	T40847	B90572	S69795	T09376
ribonuclease G [im	probable f0-f0 par	oxidoreductase, sh	glutamate-ammonia	high-affinity zinc	hypothetical prote	probable membrane	hexosephosphate tr	hexose phosphate t	protein F2D10.32 [ribosomal protein	CDA peptide synthe	probable rRNA biog	lipoprotein (impor	UTP-hexose-1-phosp	hypothetical prote

ALIGNMENTS

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B8 YVHADDVEFVPGESLKWNVRNLDVWPIFETLALRLVLQGDVIWLRCVPELRVDYTS 143	Qy 61 YVHADDVEFVPGESLKWNVRNLDVMPIFETLALRLVLQGDVIWLRCVPELRVDYTS 116	Qy 1 AGEDALRPWKSTAKHPWFQIEDNRCYIDNGKLFARGSIVGNMSRFVFDPKADYGGVGENL 60	Query Match 100.0%; Score 629; DB 1; Length 199; Best Local Similarity 100.0%; Pred. No. 5.8e-58; Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	A;Gene: nQurz C;Superfamily: cytomegalovirus HQLF2 protein C;Keywords: glycoprotein; transmembrane protein F;1-25/Domain: signal sequence #status predicted <sig> F;26-199/Product: hypothetical protein US2 #status predicted <mat> F;161-186/Domain: transmembrane #status predicted <tmm> F;68/Binding site: carbohydrate (Asn) (covalent) #status predicted</tmm></mat></sig>	MBL Data Library,	erence	A;Status; nucleic acid sequence not shown; translation not shown A:Molecule type. DNA	M.; Barrell, B.G. Curr. Top. Microbiol. Immunol. 154, 125-169, (1990) A;Title: Analysis of the protein-coding content of the sequence of human cytomegalovirus	R;Chee, M.S.; Bankier, A.T.; Beck, S.; Bohni, R.; Brown, C.M.; Cerny, R.; Horsnell, T.; F	A;Residues: (1-199) <wes> A;Cross-references: EMBL:X04650; NID:g59801; PIDN:CAB37096.1; PID:g4456177 A:Experimental source: strain AD169</wes>	A; Molecule type: DNA	A;Title: Sequence of the short unique region, short repeats, and part of the long repeats A;Reference number: A92935; MUID:87169717; PMID:3031311	Sep-1989 #sequence revision 30-Sep-1989 # # # # # # # # # # # # # # # # # #	N;Alternate names: hypothetical protein US2 C:Species: human cytomegalovirus, human herpesvirus 5	RESULT 1 QQBEC5 HOLF2 protein precursor – human cytomegalovirus (strain AD169)

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HQLF1 precursor - human cytomegalovirus (strain AD169)
N;Alternate names: hypothetical protein US3
C;Species: human cytomegalovirus, human herpesvirus 5
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 28-Jul-2000
C;Date: 30-Sep-1989 #so9917
C;Accession: F26078; S09917
R;Weston, K.; Barrell, B.G.
J. Mol. Biol. 192, 177-208, 1986
A;Title: Sequence of the short unique region, short repeats, and part of the A;Reference number: A92935; MUID:87169717; PMID:3031311
A;Accession: F26078
                                                                                                                                                                                                                                                                                                                                                                                                     probable N-acetylmuramoyl-L-alanine amidase [imported] - Yersinia pestis (strain CO9
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C;Accession: AD0205
C;Accession: AD0205
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barre, Nature 413, 523-527, 2001
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A;Experimental source: strain AD169
A;Note: this sequence was submitted to the EMBL Data Library, December 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:X04650; NID:g59801; PIDN:CAB37097.1; PID:g4456178
A;Experimental source: strain AD169
R;Chee, M.S.; Bankier, A.T.; Beck, S.; Bohni, R.; Brown, C.M.; Cerny, R.; Horsnell,
M.; Barrell, B.G.
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A;Residues: 1-254 <KUR>
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A;Residues: 1-186 <CHE>
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A;Residues: 1-186 <WES>
                                                                                                                                                                                                                                                                                                  A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                 A; Accession: AD0205
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                                                                                                                                                                                                                Cross-references: GB:AL590842; PIDN:CAC90504.1;
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PWKS---TAKHPWFQIEDNRCYIDN--GKLFARGSIVGNMSRFVFDPKADYGGVGENLYV
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Pred. No. 0.01
24; Mismatches
                                                                               Pred.
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                                                     13;
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A; Molecule type: DNA
A; Residues: 1-703 <SCH>
A; Accession: S26593
A; Molecule type: protein
A; Residues: 30-52 <SC2>
C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 4
T21532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
ALBSX1
                                                                                                                                                                       A;Description: catalyzes the breaking and reformation of 1,4-alpha-D-glucopyranosyl bonds A;Note: can also catalyze the disproportionation transfer of 6 to 8 1,4-alpha-D-glucopyra C;Superfamily: cyclomaltodextrin glucanotransferase; alpha-amylase core homology C;Keywords: calcium; duplication; extracellular protein; glycosyltransferase; hexosyltran F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-703/Product: cyclomaltodextrin glucanotransferase #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N;Alternate names: cyclodextrin glycosyltransferase
C;Species: Bacillus sp.
C;Date: 31-Mar-1993 #text_change 24-Apr-1998
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 24-Apr-1998
C;Accession: S26399; S26593
R;Schmid, G.; Englbrecht, A.; Schmid, D.
in Proceedings of the Fourth International Symposium on Cyclodextrins, Huber, O., and in Proceedings and nucleotide sequence of a cyclodextrin glycosyltransferase gene fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, May 1996 A;Reference number: Z19435 A;Accession: T21532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Berks,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein F28H7.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
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                                                                                                                      F;30-703/Product: cycloma
F;30-160/Domain: A1 <DA1>
F;161-224/Domain: B <DOB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Introns: 83/2; 147/1; 180/3; 231/3; 299/3; 364/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:Z72508; PIDN:CAA96643.1; GSPDB:GN00023; CESP:F28H7.7 A;Experimental source: clone F28H7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Accession: S26399
A;Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cyclomaltodextrin glucanotransferase (EC 2.4.1.19) precursor - N;Alternate_names: cyclodextrin glycosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-415 <WIL>
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                                                                       F;219-353/Domain: alpha-amylase F;225-428/Domain: A2 <DA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: S26399
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                                                 429-516/Domain:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENLYVHADDVEFVPGESLKWNVRNLDVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RKWELTTQ-PWLNCTDGKHCFSKMIVNNQKVLQMMIHDVGEYNGNYQTLILDPKIGY---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----IRHYRDVNMG----KWWVRNKDVL 382
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12.5%;
29.2%;
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                                                                                                  core homology <AMY:
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Pred. No. 2.
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R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Isawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001

A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 A;Reference number: A98629; MUID:21156231; PMID:11258796

A;Accession: A98950
                                                                                                                                                                                                                                                                                                                C;Species: Bscherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C;Accession: A98950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: E72384
                                                                   A;Cross-references: GB:BA000007; PIDN:BAB35992.1; PID:g13362037; A;Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                               A; Molecule type: DNA
A; Residues: 1-261 <HAY>
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                                                                                                                                                           A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R,Nelson, K.E.; Clayton,
Garrett, M.M.; Stewart,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: E72384
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                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein ECs2569 [imported] - Escherichia coli (strain O157:H7, substrain
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 Superfamily:
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pecies: Thermotoga maritima
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QIEDNRCYIDNGKLFARG-----SIVGNMSRFVFDPKAD----YGGVGENLYVHADDVE 68
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conserved hypothetical protein HI0360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.0%; Score 75.5; 32.3%; Pred. No. 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hi Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Riller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamou Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7. A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: E85798
                                                                                                                                                                                                                                                                                                                                                                                A; Gene: yebI
C; Superfamily: conserved hypothetical protein HI0360
C; Keywords: transmembrane protein; transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: The complete genome sequence of Escherichia coli
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: C64948
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R;Blattner, F.R.; Plunkett I.
A.; Rose, D.J.; Mau, B.; Sh
Science 277, 1453-1462, 1997
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A;Cross-references: GB:AE005174; NID:g12515915; PIDN:AAG56849.1;
A;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                               F;11-27/Domain: transmembrane #status predicted <TM1>
F;38-54/Domain: transmembrane #status predicted <TM2>
F;58-74/Domain: transmembrane #status predicted <TM3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:AE000280; GB:U00096; NID:g1788163; PIDN:AAC74929.1; PID:g1788166;
A;Experimental source: strain K-12, substrain MG1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-261 < BLAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable membrane protein yebI - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C64948
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C;Superfamily: conserved hypothetical protein HI0360
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                                                                                                                                                                                                                                                               F;85-101/Domain: transmembrane #status predicted <TM4>
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                                                                                                                                                                                                                               F;127-143/Domain: transmembrane
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Best Local S
Matches 13
                                                                                                                                     ;213-229/Domain:
;240-256/Domain:
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                                                            Query Match
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  l Similarity
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11.8%;
llarity 40.6%;
Conservative
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transmembrane
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#status predicted
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Pred. No. 3.8;
8; Mismatches
Score 74; DB Pred. No. 3.8; 8; Mismatches
  8;
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Pred. No. 3.8;
8; Mismatches 1
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3.8;
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Potamousis,
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A; Map position: cir
C; Superfamily: Syno
                                                                                                                                                                                                                                                                                                                           A;Title: Genome Sequence of the Plant Pathogen and Biotechnology A;Reference number: A97359; MUID:21608551; PMID:11743194 A;Accession: F97631
                                                                                                                                                                                                                                                                                                                                                                                   R;Goodner, B.; Hinkle, G.; Gattung, S.;
A.; Liu, F.; Wollam, C.; Allinger, M.;
Science 294, 2323-2328, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AI2854
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                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-360 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein AGR C_4118 [imported] - Agrobacterium tumefaciens (strain C;Species: Agrobacterium tumefaciens C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002 C;Accession: F97631
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C; Superfamily: S
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Best Local S
Matches 17
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;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
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Best Local (
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                                                                                                                                                               Superfamily: Synechocystis hypothetical protein slr1087
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17; Conserv
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                                      KSTAKHPWFQIEDNRCYIDNGKLFARGSIVGNMSRFVFDPKADYGGVGENLYVHADDVEF 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.8%; Score 74; DB: 26.6%; Pred. No. 5.5; tive 12; Mismatches
                                                                                                    11.8%; Score 74; DB 2; Length 360, 26.6%; Pred. No. 5.5;
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                                                                                                                                                                                                                                                                                                                                                                                                        Miller, N.; Blanchard, M.; Qurollo, B.; Goldi
Doughty, D.; Scott, C.; Lappas, C.; Markelz,
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     IDNIESLAFGPVVD---
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kelz, B.;
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A;Molecule type: DNA
A;Residues: 1-1409 <MOUS
A;Residues: 1-1409 <MOUS
A;Cross-references: GB:M11240; NID:g158615; PIDN:AAA74497.1; PID:g950318
A;Cross-references: GB:M11240; NID:g158615; PIDN:AAA74497.1; PID:g950318
A;Cross-references: 17, 2134, 1989
A;Title: The nucleotide sequence of Drosophila melanogaster copia-specific 2.1-kb mRNA.
A;Reference number: S03612; MUID:89183629; PMID:2538806
A;Accession: S03612
A;Accession: S03612
A;Accession: S03612
A;Cross-references: mRNA
A;Residues: 1-391,1375-1409 <MIL>
A;Cross-references: EMBL:X13719; NID:g7745; PIDN:CAA31997.1; PID:g7746
A;Cross-references: EMBL:X13719; NID:g7745; PIDN:CAA31997.1; PID:g7746
A;Cross-references: EMBL:X13719; NID:g7745; PIDN:CAA31997.1; PID:g7746
A;Cross-references: S14835; MUID:90151630; PMID:1689241
A;Accession: S14835; MUID:90151630; PMID:1689241
A;Accession: S14835; MUID:90151630; PMID:1689241
A;Accession: S14835; MUID:90151630; PMID:1689241
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DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Reference number: A71000; MUID:98344137; PMID:9679194
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C;Species: Pyrococcus horikoshii
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C;Accession: E71208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      copia polyprotein - fruit fly (Drosophila melanogaster) retrotransposon copia N;Contains: copia protein, 31K; copia protein, 48K; proteinase C;Species: Drosophila melanogaster C;Date: 04-Dec-1986 #sequence revision 04-Dec-1986 #text_change 16-Jul-1999 C;Accession: A03324; S03612; S14835
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C;Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ1207
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A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Mount, S.M.; Rubin, G.M.
Mol. Cell. Biol. 5, 1630-1638, 1985
A;Title: Complete nucleotide sequence of the Drosophila transposable element copia: homol
A;Reference number: A03324; MUID:85267679; PMID:2410772
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                                      A; Molecule type: DNA
A; Residues: 1-391, 1375-1409 < YOS>
A;Cross-references: EMBL:X54147; NID:g7749; PIDN:CAA38086.1;
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Matches 22
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22; Conservative
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%; Pred. No. 3;
12; Mismatches
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           PID: 97750
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Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; ALLOS.
Ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
                                                                                                                                                                                                                       R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, ; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           맑
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                                                                                                                                                                                                                                                                                                                                                  phosphomannose isomerase [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
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                        A;Molecule type: DNA
A;Residues: 1-394 <KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Species: Yersinia pestis
Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
Cross-references: GB:AE008689; PIDN:AAL44124.1; PID:g17741695; GSPDB:GN00187
                                                                                                                                                                                                                                                                                                                               Accession: AF2963
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Best Local Similarity
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                                                                                                                                                                                                 Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.3%; Score 71; DB 28.2%; Pred. No. 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.4%; Score 72;
23.5%; Pred. No.
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                                                                                                                                                                                                                                                                              L.; Wood, G.E.; Chen, Y.; Woo, in, T.; Levy, R.; Li, M.; McClel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34;
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A;Experimental source: strain C58 C;Genetics:
A;Gene: Atu3311
A;Map position: linear chromosome
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Best Local Similarity
                                                                                                                  Matches
134 QAAASLPERKDEMRVRALDILAILE 158
                           65 DDVEFVPGESLKWNVRNLDVMPIFE 89
                                                         82 PWKDALSHGLSWFE----KVYRLENG---LYGNLADQTGRLI-DPSFDLYNQAFALFAAA 133
                                                                                                                  23;
                                                                                    8 PWKSTAKH--PWFQIEDNRCY-IDNGKLFARGSIVGNMSRFVFDPKADYGGVGENLYVHA 64
                                                                                                                  Conservative
                                                                                                                             11.2%;
                                                                                                                  12;
                                                                                                                               Score 70.5;
Pred. No. 1
                                                                                                                                                                                                                     (Dupont)
                                                                                                                 Mismatches
                                                                                                                                  14;
                                                                                                                                            DB 2;
                                                                                                                  39;
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Search completed: January 22, 2004, 11:42:39 Job time: 23.3788 secs

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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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117.5
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109.5
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seq length: 2000000000
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      777136 seqs, 206736638 residues
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

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6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
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6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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4 US-10-029-009-20
US-10-029-009-32-5
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5 US-10-044-539-32-5
6 US-10-044-539-32-5
7 US-10-029-009-34
7 US-09-766-378A-36
7 US-09-927-122-3
7 US-09-927-122-3
7 US-09-927-121B-3
7 US-09-927-121B-3
7 US-09-927-121B-3
7 US-09-927-121B-3
7 US-10-361-849-8
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Sequence 3, 1
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Sequence 24,
Sequence 10,
Sequence 10,
Sequence 26,
Sequence 19, Appl
Sequence 20, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 325, App
Sequence 34, Appl
Sequence 34, Appl
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 24, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 10, Appl
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ALIGNMENTS

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8.0		8.0		8.1	8.1		8.1	8.1	8.1	8.1	8.1	8.3	8.3	8.7	8.7	9.1	9.6	٠	10.2	0		10.5	0		0	0			10.8
267	248	248	358	358	316	316	316	316	316	316	316	3931	329	1938	893	6291	41	41	21	20	394	394	104	61	41	41	260	260	129
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US-10-131-409-83	US-10-150-811-85	US-10-131-409-85	US-09-925-299-923	US-09-925-299-923	US-10-017-754-340	US-10-113-872-340	US-10-274-375-3	US-09-476-300-340	US-09-849-626-340	US-09-902-941-340	US-09-736-457-340	US-10-120-801-18	US-10-104-047-3709	US-10-014-436-2	US-10-014-436-4	US-10-329-079-41	US-10-410-842A-69	US-10-410-842A-56	US-10-133-973-74	US-10-029-009-12	US-10-410-842A-2	US-10-369-300-13	US-10-410-842A-6	US-10-410-842A-30	US-10-410-842A-44	US-10-410-842A-40	US-10-264-634-39	US-10-264-634-23	US-10-152-190-6
83,	, 85	е В	e 923,	,		34	Sequence 3, Appli	34	34	Sequence 340, App	34(Sequence 18, Appl	3709	'n	Sequence 4, Appli	41,	Sequence 69, Appl	56,	•	12	Sequence 2, Appli	Sequence 13, Appl	6	30	44	e 40	39	23	Sequence 6, Appli

SOFTWARE: PatentIn version 3.1 SEQ ID NO 19 LENGTH: 199 TYPE: PRT ORGANISM: human cytomegalovirus Towne strain US2 US-10-300-393-19 US-10-300-393-19 Sequence 19, Application US/10300393 Publication No. US20030118568A1 GENERAL INFORMATION: Query Match 78.1%; Score 740; DB 15; Length 199; Best Local Similarity 100.0%; Pred. No. 1.5e-77; Matches 136; Conservative 0; Mismatches 0; Indels APPLICANT: Crew, Mark D. TITLE OF INVENTION: Viral Stealth Technology to Prevent T-Cell-Mediated Rejection TITLE OF INVENTION: Xenografts FILE REFERENCE: 8793-50391 CURRENT APPLICATION NUMBER: US/10/300,393 CURRENT FILING DATE: 2002-11-19 PRIOR APPLICATION NUMBER: US 60/342,981 PRIOR FILING DATE: 2001-12-18 NUMBER OF SEQ ID NOS: 22 142 140 08 82 20 22 DYTSSAYMWNMQYGMV 157 YGGVGENLYVHADDVEFVPGESLKWNVRNLDVMPIFETLALRLVLQGDVIWLRCVPELRV 141 RLPDGITKAGEDALRPWKSTAKHPWFQIEDNRCYIDNGKLFARGSIVGNMSRFVFDPKAD DYTSSAYMWNMQYGMV 155 RLPDGITKAGEDALRPWKSTAKHPWFQIEDNRCYIDNGKLFARGSIVGNMSRFVFDPKAD YGGVGENLYVHADDVEFVPGESLKWNVRNLDVMPIFETLALRLVLQGDVIWLRCVPELRV 0; Gaps 139 79 81 0,

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US-10-029-009-20
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APPLICANT: Annis, David Allen
APPLICANT: Kalghatgi, Krishna
APPLICANT: Kalghatgi, Krishna
APPLICANT: Nash, Huw M.
TITLE OF INVENTION: Affinity Selection-Based Screening of Hydrophobic Proteins
FILE REFERENCE: 111025.173 US2
CURRENT APPLICATION NUMBER: US/10/029,009
CURRENT FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: US 60/258,970
PRIOR FILING DATE: 2000-12-29
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 20, Application US/10300393
Publication No. US20030118568A1
GENERAL INFORMATION:
APPLICANT: Crew, Mark D.
TITLE OF INVENTION: Viral Stealth Technology to Prevent T-Cell-Mediated Rejection of TITLE OF INVENTION: Xenografts
FILE REFERENCE: 8793-50391
                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.1
SEQ ID NO 20
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                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/300,393
CURRENT FILING DATE: 2002-11-19
PRIOR APPLICATION NUMBER: US 60/342,981
PRIOR FILING DATE: 2001-12-18
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                                                                                                                         10 VFMVVYISYIYARLPDGITKAGEDALRPWKSTAKHPWFQIEDNRCYIDNGKLFARGSIVG
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                                                                                      4 VLVLAILAVLFLRLADSVPRPLDVVV----SEIRSAHFRVEENQCWSHMGMLHYKGRMSG
NFTEKHFVSVGIVSQSYMDRLQVSGEQYHHDE----RGAYFEWNIGGHPVPHTVDMVDI
                                            NMSR-----FVFDPKADYGGVGENLYVHADDVEFVPGESLKWNV-----RNLDVMPI 116
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No. US20020164617A1
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                                                                                                                                                                             12.1%; Score 115; DB 15; 24.1%; Pred. No. 4.9e-05; tive 32; Mismatches 60;
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; LENGTH: 498
; TYPE: PRT
; ORGANISM: Human
US-10-029-009-22
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Best Local Similarity
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SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT APPLICATION NUMBER: US/10/029,009
CURRENT FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: US 60/258,970
PRIOR FILING DATE: 2000-12-29
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APPLICANT: Annis, David Allen
APPLICANT: Kalghatgi, Krishna
APPLICANT: Nash, Huw M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/044,692
FILING DATE: 11-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/912,951
APPLICATION NUMBER: US 08/854,050
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKFLVNVÄLVFMVVYISYIYARLPDGITKAGEDA------LRPWKSTÄKHPW 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --TLSTR---WGDPKKYAACVPQVRMDYSSHTINWYLQ 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MKFLVNVALVFMVVYISYIYADYKDDDDKMNTSAPPAVSPNITVLAP----GKGPW 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FETLALRIVLOGD-VIWLRCVPELRVDYTSSAYMWNMQ 153
                                                                                                                                                                                                                                                                                                                                                 CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                             COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                            STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nakamura, Toru
Chapman, Karen B.
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/10029009
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cech, Thomas R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ingner, Joachim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THERAPEUTIC METHODS
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Pred. No. 0.00071;
0; Mismatches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 14;
                                                                                                                                                                                              Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 498;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14;
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RESULT 6
US-10-044-539-325
; Sequence 325, App
; Publication No. U
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 325:
US-10-044-692-325
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SEQUENCE CHARACTERISTICS:
LENGTH: 1189 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 11.6%; Score 109.5; DB 15; Local Similarity 32.1%; Pred. No. 0.0026;
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/044,539
FILING DATE: 11-Jan-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 01:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT:
THERAPEUTIC METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 RAPRCRAVRSLLRSHYREVLPLATEV----RRLGPQGWRLVQRGDPAAFRALVAQCLVCV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50 EDNRCYIDNGKLFARGSIVGNMSRFVFDPKADYGGVGENLYVHADDVEF------V 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MKFLVNVALVFMVVYISYIYAD-PSSRSAAGTMEFAAASTQRCVLLRTWEALAPATPAMP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PGESLKWNVRNLDVMPIFETLALRLVLQGDVIWLRC 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
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                                                                                                                                                                                                                                    CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                               ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                           COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/10044539
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Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cech, Thomas R.
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                                                                               #1.30
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                                             US-10-029-009-34
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Publication No. US20020164617A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version SEQ ID NO 34
Query Match
                                                                                                                                                                                                                                  TITLE OF INVENTION: Affinity Selection-Based Screening of Hydrophobic Proteins FILE REFERENCE: 111025.173 US2
CURRENT APPLICATION NUMBER: US/10/029,009
CURRENT FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: US 60/258,970
PRIOR FILING DATE: 2000-12-29
                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Felsch, Jason S.
APPLICANT: Annis, David Allen
APPLICANT: Kalghatgi, Krishna
APPLICANT: Nash, Huw M.
                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (415) 576-03 INFORMATION FOR SEQ ID NO: 325:
                                                                                    ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                  TYPE: PRT
                                                                 OTHER INFORMATION: Met-Melitin SS-FLAG M1 tag-m2 mAchR sequence
                                                                                                                                                    ENGTH: 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Apple, Randolph T.

REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-002600US

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 325:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 RAPRCRAVRSILRSHYREVLPLATFV----RRLGPQGWRLVQRGDPAAFRALVAQCLVCV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKFLVNVALVFMVVYISYIYAD-PSSRSAAGTMEFAAASTQRCVLLRTWEALAPATPAMP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P----WDARPPPAAPSFROVSCLKELVARVLORLC 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PGESLKWNVRNLDVMPIFETLALRLVLQGDVIWLRC 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/912,951 FILING DATE: <Unknown>
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APPLICATION NUMBER: US 08/844,419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/851,843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/854,050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENGTH: 1189 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPLICATION NUMBER: US 08/846,017
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.6%; Score 109.5; DB 32.1%; Pred. No. 0.0026;
     11.0%;
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     Score 104;
     DB 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65;
     Length 496;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1189;
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; MOLECULE TYPE: protein ; SEQUENCE DESCRIPTION: SEQ ID NO: 36: US-09-766-378A-36
                                                                       US-09-927-122-3
                                                                                            RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-766-378A-36
Sequence 3, Application US/09927122 Publication No. US20030012782A1 GENERAL INFORMATION: APPLICANT: GOLD, DANIEL P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASELSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/766,378A
FILING DATE: 19-Jan-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:

NAME: COrless, Peter F
REGISTRATION NUMBER: 33,860
REFERENCE/DOCKET NUMBER: 4800:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jiao, Jin-an
Wong, Hing C.
TITLE OF INVENTION: SOLUBLE MHC COMPLEXES !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKFLVNVALVFMVVYISYIYARLPD
                                                                                                                                                                                                                        l Similarity
21; Conserv
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                                                                                                                                               MKFLVNVALVFMVVYISYIYA 21
                                                                                                                                                                                    MKFLVNVALVFMVVYISYIYA 21
                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 21 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/960,190 FILING DATE: 29-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: MA
                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: usa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nilarity 88.0%; Pred. No. 0.0035;
Conservative 0; Mismatches
                                                                                                                                                                                                                       10.8%; Score 102; DB 9; llarity 100.0%; Pred. No. 8.4e-05; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rhode, Peter R.
Acevedo, Jorge
Burkhardt, Martin
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; Sequence 8, Application US/10361849
; Publication No. US20030170619A1
; GENERAL INFORMATION:
; APPLICANT: Hara, Toshio
; TITLE OF INVENTION: Nucleic Acid Capable of Promoting Gene Expression
; FILE REFERENCE: 027847.00102US01
; CURRENT APPLICATION NUMBER: US/10/361,849
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: 60/355,752
; PRIOR FILING DATE: 2002-02-12
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; EQ ID NO 8
; LENGTH: 21
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APPLICANT: SHOPES, ROBERT J.

TITLE OF INVENTION: METHOD AND COMPOSITION FOR ALTERING A B

TITLE OF INVENTION: PATHOLOGY

FILE REFERENCE: 032077.0003

CURRENT APPLICATION NUMBER: US/09/927,121B

CURRENT FILING DATE: 2001-08-10

NUMBER OF SEQ ID NOS: 93

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 3

LENGTH: 21

TYPE: PRT

ORGANISM: Apis mellifera
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Best Local S
Matches 21
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Best Local Sim
Matches 21;
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LENGTH: 21
TYPE: PRT
ORGANISM: Apis mellifera
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TITLE OF INVENTION: METHOD AND COMPOSITION FOR ALTERING A T CELL MEDIATED TITLE OF INVENTION: PATHOLOGY FILE REFERENCE: 032077.0002
CURRENT APPLICATION UMBER: US/09/927,122
CURRENT FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patentin Ver. 2.1
 Query Match
                                                         TYPE: PRT
ORGANISM: Apis mellifera
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100.0%; Pred. No. 8.4e-05;
tive 0; Mismatches 0;
 10.8%;
Score 102;
 DB 12;
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Length 21;
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US-10-256-977-10
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Publication No.
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TITLE OF INVENTION: Affinity Selection-Based Screening of Hydrophobic Proteins
FILE REFERENCE: 111025.173 US2
CURRENT APPLICATION NUMBER: US/10/029,009
CURRENT FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: US 60/258,970
PRIOR FILING DATE: 2000-12-29
NUMBER OF SEQ ID NOS: 34
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                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/256,977
CURRENT FILING DATE: 2002-09-27
PRIOR APPLICATION NUMBER: US/10/084,298
                                                                                                                                                                             PRIOR FILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: 60/270,823
PRIOR FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 60/281,353
PRIOR FILING DATE: 2001-04-03
                                                   SOFTWARE: P
                                                                                         NUMBER OF SEQ ID NOS:
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TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                            ITLE OF INVENTION: Composition and Method for Treating Inflammatory ITLE OF INVENTION: Disorders ILE REFERENCE: GI5358 CIP
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ORGANISM: Artificial Sequence
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                                                                                                         FILING DATE: 2000-04-28
                                                                                                                                          APPLICATION NUMBER: 60/131,473 FILING DATE: 1999-04-28
                                                                                                                          APPLICATION NUMBER: 09/561,811
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                                                                      PatentIn Ver.
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Annis, David Allen
Kalghatgi, Krishna
Nash, Huw M.
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Fouser, Lynette
Spaulding, Vikki
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vo. US20020164617A1
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APPLICANT: Zhang, Ke
APPLICANT: Zhu, Daocheng
ITITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
ITITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES
FILE REFERENCE: UC67.002A
CURRENT APPLICATION NUMBER: US/09/847,208
CURRENT FILING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 177
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26
LENGTH: 70
TYPE: PRT
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; OTHER INFORMATION: Description of Artificial Sequence: Amino acid tag
US-10-256-977-10
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; Sequence 26, Application US/09847208

; Publication No. US20030082190A1
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LENGTH: 49
TYPE: PRT
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Best Local Similarity 100.0%; P
Matches 21; Conservative 0;
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PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/131,473
PRIOR APPLICATION NUMBER: 60/131,473
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TITLE OF INVENTION: Disorders
FILE REFERENCE: G15358 CIP
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OTHER INFORMATION: Description of Artificial Sequence: Amino acid tag
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21; Conservative
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Fouser, Lynette
Spaulding, Vikki
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| ORGANISM: Apis mellifera(Honeybee) | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | Do. 2-2-203-26 | D
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Maximum Match 100%
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Perfect score:
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  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*
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US-08-960-190A-36
US-08-93-76-330-4
US-08-499-568-2
US-08-793-958-11
US-08-793-958-11
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US-08-974-549A-613
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Sequence 3, Appli	Sequence 2, Appli	Sequence 27542, A	Sequence 12, Appl	Sequence 3, Appli	Sequence 13, Appl	Sequence 11, Appl	Sequence 84, Appl	Sequence 6181, Ap	Sequence 28582, A	Sequence 4, Appli	Sequence 76, Appl	Sequence 340, App	Sequence 340, App	Sequence 32535, A	Sequence 17381, A	Sequence 71, Appl	Sequence 2, Appli

ALIGNMENTS

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
APPLICATION NUMBER: US 08/844,419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Ca
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                                                                                                                                                                                                                     FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                         APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
                 FILING DATE: 14-AUG-1997 PRIOR APPLICATION DATA:
                                                                                 FILING DATE: 09-MAY-PRIOR APPLICATION DATA:
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                                                             APPLICATION NUMBER:
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ZIP: 94111-3834
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18-APR-1997
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Best Local Similarity
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FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
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LENGTH: 1189 amino aci
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                            APPLICANT: Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT:
TITLE OF INVENTION: THERAPEUTIC METHODS
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APPLICATION NUMBER:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
                                                                                                CITY: San Francisco
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                                                           COUNTRY:
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LICATION NUMBER: WO PCT/US97/17618
ING DATE: 01-OCT-1997
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Chapman, Karen B.
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Harley, Calvin
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hTRT protein"
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Best Local Similarity
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APPLICANT: Rhode,
APPLICANT: Aceved
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,951
FILING DATE: 14-AUG-1997
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APPLICANT:
APPLICANT:
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APPLICATION NUMBER: U
FILING DATE: 01-OCT-1
CLASSIFICATION: 435
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PRIOR APPLICATION DATA:
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PRIOR APPLICATION NUMBER: US 08/851,843
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 0 FILING DATE: 09-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 18-APR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Apple, Rando. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 06-MAY-1997
                                                                                                                                                                                                                                                                                                            116
                                                                                                                                                                                                                                                                                                                                              100 PGESLKWNVRNLDVMPIFETLALRLVLQGDVIWLRC 135
                                                                                                                                                                                                                                                                                                                                                                                                                  50 EDNRCYIDNGKLFARGSIVGNMSRFVFDPKADYGGVGENLYVHADDVEF------V
F: Acevedo, Jorye
F: Acevedo, Jorye
T: Burkhardt, Martin
IT: Jiao, Jin-an
NT: Wong, Hing C.
NF INVENTION: SOLUBLE MHC COMPLEXES AND
DF INVENTION: METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKFLYNVALVFMVVYISYIYARLPDGITKAG--EDA-----LRPWKSTAKHPWFQI 49
                                                                                                                                                                                                                                                                                                                                                                                 RAPRCRAVRSLLRSHYREVLPLATFV----RRLGPQGWRLVQRGDPAAFRALVAQCLVCV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MKFLVNVALVFMVVYISYIYAD-PSSRSAAGTMEFAAASTQRCVLLRTWEALAPATPAMP 59
                                                                                                                                                                                                                                                                                                          P----WDARPPPAAPSFRQVSCLKELVARVLQRLC 146
                                                                                                                                                                                                                  Application US/08960190A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1189 amino acids
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                                                                                                                                                           Rhode, Peter R.
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18-APR-1997
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n Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.6%; Score 109.5; DB 4; 32.1%; Pred. No. 0.00063; tive 10; Mismatches 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US 08/854,050
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TITLE OF INVENTION:

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; LENGTH: 21
; TYPE: PRT
; ORGANISM: Melittin Signal Peptide sequence
US-09-376-330-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-960-190A-36
                                          Query Match
Best Local
                              Matches
                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/376,330
CURRENT FILING DATE: 1999-08-18
NUMBER OF SEQ ID NOS: 35
                                                                                                                                                                                                                          APPLICANT: Thomas, David Y.
TITLE OF INVENTION: Method for screening for
TITLE OF INVENTION: UDP-glucose:glycoprotein glucosyltransferase (UGGT) activity
TITLE OF INVENTION: and nucleic acid encoding for UGGT
FILE REFERENCE: 2139-9"US"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                   PPLICANT: Tessier, Daniel C.
                                                                                                                                                                                                                                                                                                                                                                  tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Corless, Peter F
REGISTRATION NUMBER: 33,860
REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/960,190A FILING DATE: 29-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: us
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LASSIFICATION: 536
OR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                4, Application US/09376330
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1 MKFLVNVALVFMVVYISYIYA 21
                                           Similarity
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Bergeron, John J.M.
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130 Water Street
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                              Conservative
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                                          10.8%;
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                                          Score 102; DB 4;
Pred. No. 1.2e-05;
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                             Mismatches
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                                                        Length 21;
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US-08-793-958-2
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                                           STREET:
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US-08-499-568-2
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APPLICANT: Cohen, (
APPLICANT: Bisenbe:
APPLICANT: Nicola,
                                                                                                                          GENERAL INFORMATION:
APPLICANT: Cohen, (
APPLICANT: Eisenber
APPLICANT: Nicola,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (312) 474-04-
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                     guence 2, Applic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: No. 5654174and, Gr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
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                                                           CORRESPONDENCE ADDRESS:
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                                                                             UMBER OF SEQUENCES:
                                                                                             ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                             Local Similarity nes 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid TOPOLOGY: linear
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STATE: Illinois
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 60606
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                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
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Chicago
: Illinois
                                                                                                                                                                                                    Application US/08793958
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                                6300 Sears Tower,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 S. Wacker Drive
                                                                                                                        Nicola, Anthony
                                                                                                                                           Eisenberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (312) 474-0448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eisenberg,
                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                      Cohen, Gary H.
                                                Marshall,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
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                                                                                             Herpes Simplex Virus
Variants
                                                                                                                                                                                                                                                                                                                                                             10.5%; Score 99;
100.0%; Pred. No
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                                O'Toole, (
                                                                                                                                        Roselyn J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35,302
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                                Gerstein, Murray & Borun
S. Wacker Drive
                                                                                                                                                                                                                                                                                                                                                               No.
                                                                                                                                                                                                                                                                                                                                                                              DB 1;
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                                                                                                            Glycoprotein
                                                                                                                                                                                                                                                                                                                                                                              Length 308
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy

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Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08139609
Patent No. 5837249
GENERAL INFORMATION:
APPLICANT: Heber-Katz, Ellen
APPLICANT: Dietzschold, Bernhard
TITLE OF INVENTION: Method for Generating an
TITLE OF INVENTION: Cell Response Protective
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/868,946
FILING DATE: 15-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/685,459
FILING DATE: 12-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/047,443
FILING DATE: 08-MAY-1987
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 308 amino acids
                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/139,609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: NO. 5814486and, Greta E. REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32813
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid TOPOLOGY: linear
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                                                                                                                                                                          FILING DATE:
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                  ZIP: 19477
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T: Spring House Corporat
Spring House
                                                                                                                                                                                                                                                                                                                                                                                            Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                           USA
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; Pred. No. 0.0015;
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Against a Virus
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; Sequence 11, Application US/08499568; Patent No. 5654174; GENERAL INFORMATION: APPLICANT: Cohen, Gary H. APPLICANT: Eisenberg, Roselyn J. APPLICANT: Nicola, Anthony TITLE OF INVENTION: Herpes Simplex; TITLE OF INVENTION: Variants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
5470718-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5470718-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 561,553
FILING DATE: 01-AUG-1990
SEQ ID NO:5:
                                                                                                                                                                                                                                                                                                                              US-08-499-568-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;Patent No. 5470718
; APPLICANT: O'CALLAGHAN, DENNIS J.
; TITLE OF INVENTION: EQUINE HERPESVIRUS TYPE 1 GLYCOPROTEIN
;D NUCLEIC ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 19; Conserv
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 369 amino acids
TYPE: amino acid
TOPOLOGY: unknown
                                                   STREET: Chicago CITY: Chicago Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/954,417
FILING DATE: 30-SEP-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: WS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US OF FILING DATE: 19-APR-1985 ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                             NUMBER OF SEQUENCES: 1
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   y Match 10.5%; Score 99; DB Local Similarity 100.0%; Pred. No. 0.0 hes 19; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Bak, Mary 5.
REGISTRATION NUMBER: 31,215
REGISTRATION NUMBER: WSTIDUSA
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                                  ZIP: 60606
                                                                                                                             ADDRESSEE:
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                                                                                                          3: Marshall, O'Toole, 6300 Sears Tower, 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.5%; Score 99; DB 6; ilarity 100.0%; Pred. No. 0.0021; Conservative 0; Mismatches 0
                                                                                                                                                                                 Herpes Simplex Virus Glycoprotein D
Variants
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                                                                                                            Gerstein, Murray & Borun
S. Wacker Drive
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US-08-793-958-11
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LENGTH: 388 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-499-568-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
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Best Local Similarity
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REFERENCE/DOCKET NUMBER: 3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (312) 474-0446
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 11:
                 TELEFAX: (312) 474-044
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                  NAME: NO. 5814486and, Greta E. REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32813
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Cohen, Gary H.
APPLICANT: Eisenberg, Rose:
APPLICANT: Nicola, Anthony
TITLE OF INVENTION: Herpes
TITLE OF INVENTION: Variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                              TELEPHONE: (312)
                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (312) 474-0448
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                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
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5814486
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6300 Sears Tower, 233 S. Wacker Drive
388 amino acids
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                                                                     474-0448
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: 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Roselyn J.
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                                   11:
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. 0.0022;
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US-08-413-118-23
; Sequence 23, Application US/08413118
; Patent No. 5688920
; GENERAL INFORMATION:
; APPLICANT: PAOLETTI, ENZO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-793-958-11
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                                                                              RESULT 12
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TELEX: 425066 CURTMS
TELEX: 425066 CURTMS
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 393 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
US-08-220-151-23
                                                                                                                                                                                     Query Match
Best Local S
Matches 19
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/220,151
FILING DATE: 30-MAR-1994
CLASSIFICATION: 435
ATTORNEY/ACCOUNT
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 45
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: NUTTITLE OF INVENTION: CANUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
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5529780
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19; Conserv
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                                                                                                                                                                                  10.5%; Score 99; llarity 100.0%; Pred. No. Conservative 0; Mismatcl
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NUCLEOTIDE AND AMINO ACID SEQUENCES OF

CANINE HERPESVIRUS GB, GC AND GD AND USES THEREFOR
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                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Version #1.25
                                                                                                                                                                                DB 1; uc., o. 0.0022; 0;
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0.0022;
                                                                                                                                                                                                                   Length 393;
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                                                                                                                                                                                      0;
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RESULT 13
US-08-473-446-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/413,118
FILING DATE: 29-MAR-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/220,151
FILING DATE: 30-MAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 393 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: CURTIS, MORRIS & SAFFOI STREET: 530 FIFTH AVENUE, 25TH FLA CITY: NEW YORK
STATE: NEW YORK
COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                    APPLICANT: PAOLETTI, ENZO
APPLICANT: LIMBACH, KEITH J.
TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES OF
TITLE OF INVENTION: CANINE HERPESVIRUS 9B, 9C, AND 9D AND USES THEREFOR NUMBER OF SEQUENCES: 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: FROMMER, WILLIAM S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2670
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: CURTIS, MORRIS & SAFFORD, P.C.
STREET: 530 FIFTH AVENUE, 25TH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
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                                                                                                                                                                             STREET: 530 FI
CITY: NEW YORK
STATE: NEW YOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                 OUNTRY:
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N-terminal
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AVENUE, 25TH FLOOR
US/08/473,446
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0.0022;
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5182195-10
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US-08-499-568-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PATENT NO. 5182195
APPLICANT: NAKAHAMA, KAZUO; KAISHO, YOSHIHIKO; YOSHIMURA, ITITLE OF INVENTION: METHOD FOR INCREASING USING PROTEASE, DEFICIENT YEASTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 09-NOV-1988
SEQ ID NO:10:
LENGTH: 393
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity Matches 19; Conserv
                                                                                                                                                                                                                                                   Sequence 4, Applic Patent No. 5654174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 393 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                            APPLICANT: Cohen, Gary H.
APPLICANT: Eisenberg, Rosely
APPLICANT: Nicola, Anthony
TITLE OF INVENTION: Herpes S
TITLE OF INVENTION: Variants
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 71
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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APPLICATION NUMBER:
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 840-3333
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: FROMMER, WILLIAM S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2670
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                                            Chicago
: Illinois
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                                                                           E: Marshall, O'Toole,
6300 Sears Tower, 233
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                                                                                                                                               Variants
                                                                                                                                                               Herpes Simplex Virus Glycoprotein
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S. Wacker Drive
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0.0022;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,568
FILING DATE:
APPLICATION NUMBER: US/08/499,568
FILING DATE:
APPLICATION NUMBER: US/08/499,568
FILING DATE:
APPLICATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 33,302
REFERENCE/DOCKET NUMBER: 33,302
REFERENCE/DOCKET NUMBER: 33,302
REFERENCE/DOCKET NUMBER: 33,302
REFERENCE/DOCKET NUMBER: 32813
TELECOMMUNICATION INFORMATION:
TELEPAX: (312) 474-6300
TELEPAX: (312) 474-6300
TELEPAX: (312) 474-6448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 394 maino acids
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 394 maino acids
TOPOLOGY: linear
WOLECULE TYPE: protein
US-08-499-568-4

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Search completed: January 22, 2004, 11:38:43

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Maximum Match 100%
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Maximum DB
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  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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  seq length: 0
seq length: 2000000000
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1: pir1:*
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Match
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Gapop 10.0 , Gapext 0.5
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 MKFLVNVALVFMVVYISYIY......GQPELAPEDPEDSALLEDPV 177
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glycoprotein D pre
glycoprotein D pre
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glycoprotein D pre
glycoprotein D pre
copia polyprotein
glycoprotein D -h
glycoprotein D pre
US6 protein -huma
copia polyprotein
peptidoglycan boun
ribosomal protein
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                                              hypothetical prote conserved hypothet hypothetical 43.7K hypothetical prote hypothetical prote beta-fructofuranos beta-fructosidase
               phosphoglycolate p
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HQLF1 precursor -
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140 DYTSSAYMWNMQYGMV 155

QBECS QBECS QBECS MAINternate names: hypothetical protein USZ Cipacies: Numan cytomegalovirus (strain AD169) MAINternate names: hypothetical protein USZ Cipacies: Numan cytomegalovirus, human herpesvirus 5 Cipacies: Numan cytomegalovirus, human herpesvirus 6 Cipacies: Numan cytomegalovirus, human herpesvirus 6 Cipacies: Numan cytomegalovirus, human herpesvirus 6 Cipacies: Numan cytomegalovirus, human herpesvirus, and part of the long reference number: Superimental source; strain AD169 Richee, M.S.; Bankler, A.T.; Beck, S.; Bohni, R.; Brown, C.M.; Cerny, R.; Horsnell, R.; Barrell, B.G. Richee, M.S.; Bankler, A.T.; Beck, S.; Bohni, R.; Brown, C.M.; Cerny, R.; Horsnell, R.; Barrell, B.G.; Bankler, A.T.; Beck, S.; Bohni, R.; Brown, C.M.; Cerny, R.; Horsnell, R.; Barrell, B.G.; Bankler, A.T.; Beck, S.; Bohni, R.; Brown, C.M.; Cerny, R.; Horsnell, R.; Barrell, B.G.; Bankler, A.T.; Beck, S.; Bohni, R.; Brown, C.M.; Cerny, R.; Horsnell, R.; Barrell, B.G.; Bankler, A.T.; Beck, S.; Bohni, R.; Brown, C.M.; Cerny, R.; Horsnell, R.; Barrell, B.G.; Barrell,	ALIGNMENTS	30 75.5 8.0 301 2 E72384 31 75.5 8.0 316 2 A59021 aldehyde reductase 32 75.5 8.0 396 2 T04224 33 75.5 8.0 527 2 C70397 34 75 7.9 394 2 AB1870 periplasmic cell d 36 74 7.8 261 2 A89950 hypothetical prote 37 74 7.8 261 2 C64948 38 74 7.8 361 2 C64948 39 74 7.8 351 2 S11237 40 74 7.8 360 2 A12854 41 74 7.8 360 2 A12854 42 74 7.8 473 1 T26280 43 73.5 7.8 757 2 B90572 45 73 7.7 463 2 D41853	
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Curr. Top. Microbiol. Immunol. 154, 125-169, 1990
A;Title: Analysis of the protein-coding content of the sequence of human cytomegalovirus A;Reference number: S09749; MUID:90269039; PMID:2161319
A;Accession: S09917
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-186 <CHE>
A;Cross-references: EMBL:X17403; NID:g59591; PIDN:CAA35314.1; PID:g1780934
A;Experimental source: strain AD169
A;Note: this sequence was submitted to the EMBL Data Library, December 1989
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: HQLF1
C;Superfamily:
C;Keywords: g1:
F;1-25/Domain:
F;26-186/Produ
F;160-182/Doma
F;60/Binding s
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J. Mol. Biol. 192, 177-208, 1986

A;Title: Sequence of the short unique region, short repeats, and A;Reference number: A92935; MUID:87169717; PMID:3031311

A;Accession: F26078
                                                                                                                                   N;Contains: melittin F
C;Species: Apis mellifera (honeybee)
C;Species: Apis mellifera (revision 19-Feb-1984 #text change 15-Sep-2000 C;Date: 19-Feb-1984 #sequence revision 19-Feb-1984 #text change 15-Sep-2000 C;Accession: A91133, A91640; B61285; S23131; A01761; A18880
C;Accession: A91135, L23-126, L983
A;Title: Nucleotide sequence of cloned cDNA coding for honeybee prepromelitt A;Reference number: A91133; MUID:83287387; PMID:6309516
A;Accession: A91133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:X04650; NID:g59801; PIDN:CAB37097.1; PID:g4456178
A;Experimental source: strain AD169
R;Chee, M.S.; Bankier, A.T.; Beck, S.; Bohni, R.; Brown, C.M.; Cerny, R.; M.; Barrell, B.G.
R;Habermann, E.; Jentsch, J.
Hoppe-Seyler's Z. Physiol. Chem. 348, 37-50,
                                                                                     A; Molecule type: mRNA
A; Residues: 1-70 < VLA>
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A;Residues: 1-186 <WES>
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Best Local S
Matches 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QLF1 precursor - human cytomegalovirus (strain AD169);Alternate names: hypothetical protein US3;Species: human cytomegalovirus, human herpesvirus 5;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 28-Jul-2000;Accession: F26078; S09917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;Superfamily: cytomegalovirus HQLF1 protein
;Keywords: glycoprotein; transmembrane protein
;1-25/Domain: signal sequence #status predicted <SIG>
;26-186/Product: hypothetical protein US3 #status predicted <MAT>
;160-182/Domain: transmembrane #status predicted <TMM>
;60/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                     Cross-references: GB:X02007; NID:g5621; PIDN:CAA26038.1; PID:g5622
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --TLSTR---WGDPKKYAACVPQVRMDYSSQTINWYLQRSM
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Pred. No. 8.9e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                    honeybee
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32;
                                                                                                                                                                                                prepromelittin.
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A;Title: Isolation and structure of N(alpha)-formyl melittin.
A;Reference number: A91267; MUID:72098669; PMID:5139483
A;Contents: annotation; synthesis
A;Note: N-formyl-melittin major was isolated from the venom and its
R;Mollay, C.; Vilas, U.; Kreil, G.
Proc. Natl. Acad. Sci. U.S.A. 79, 2260-2263, 1982
A;Title: Cleavage of honeybee prepromelittin by an endoprotease from
A;Reference number: A18880; MUID:82247982; PMID:7048315
A;Contents: annotation; intact signal sequence after cleavage by par
R;Eisenberg, D.; Gribskov, M.; Terwilliger, T.C.
submitted to the Brookhaven Protein Data Bank, October 1990
A;Reference number: A50496; PDB:2MLT
A;Contents: annotation; X-ray crystallography, 2.0 angstroms, residu
R;Terwilliger, T.C.; Eisenberg, D.
J. Biol. Chem. 257, 6010-6015, 1982
A;Title: The structure of melittin. I. Structure determination and parents annotation; X-ray crystallography, 2.0 angstroms
A;Contents: annotation; X-ray crystallography, 2.0 angstroms
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A;Molecule type: protein
A;Residues: 44-69 <RAP:
R;Residues: 44-69 <RAP:
R;Schroeder, E; Luebke, K.; Lehmann, M.; Beetz, I.
Experientia 27, 764-765, 1971
Experientia 27, 764-765, 1971
A;Title: Haemolytic activity and action on the surface tension of aqueous solutions of sya;Reference number: A91266; MUID:72098668; PMID:5139482
                                                                                                                                                                                                          A;Contents: annotation; X-ray crystallography, 2.0 angstroms C;Superfamily: melittin major C;Keywords: amidated carboxyl end; blocked amino end; hemolysis; F;1-21/Domain: signal sequence #status experimental <SIG>F;2-43/Domain: propeptide #status experimental <PRO>F;44-69/Product: melittin major #status experimental <MAJ>F;51-69/Product: melittin F #status experimental <MELF>F;44/Modified site: formylated amino end (Gly) (in mature form) (F;69/Modified site: amidated carboxyl end (Gln) (amide in mature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Kreil, G.; Kreil-Kiss, G.
Biochem. Biophys. Res. Commun. 27, 275-280, 1967
A;Title: The isolation of N-formylglycine from a polypeptide
A;Reference number: A90165; MUID:67248282; PMID:6040373
A;Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Ramalingam, K.; Bello, J.
Biochem. J. 284, 663-665, 1992
A;Title: Effect of permethylation on the haemolytic activity of melittin.
A;Reference number: S23131; MUID:92321983; PMID:1622387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Terwilliger, T.C.; Eisenberg, D.
J. Biol. Chem. 257, 6016-6022, 1982
A;Title: The structure of melittin. II. Interpretation of the A;Reference number: A30640; MUID:82189959; PMID:7076662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Note: about 10% of melittin is formylated at the R;Luebke, K.; Matthes, S.; Kloss, G. Experientia 27, 765-767, 1971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Contents: annotation; synthesis
A; Note: the structure of melittin was confirmed by synthesis of a
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J. Biochem. 83, 405-410, 1978
                                                                                                                       Similarity
MKFLVNVALVFMVVYISYIYA 21
                                                                                      Conservative
                                                                                                                 10.8%;
                                                                                   0;
                                                                                                        Score 102; Db 1,
                                                                                      Mismatches
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                                                                                      Gaps
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A;Cross-references: GB:J02217; NID:g330100; PIDN:AAA45785.1; PID:A;Experimental source: strain Patton
A;Note: a strongly hydrophobic region of 25 amino acids between 1 R;Lasky, L.A.; Dowbenko, D.J.
DNA 3, 23-29, 1984
A;Title: DNA sequence analysis of the type-common glycoprotein-D A;Reference number: A90945; MUID:84131549; PMID:6321120
A;Recession: B90945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Species: human herpesvirus 1
C; Date: 05-Apr-1983 #sequence_revision 05-Apr-1983 #text_change 16-Jul-1999
C; Accession: A94268; B90945; A03729
R; Watson, R.J.; Weis, J.H.; Salstrom, J.S.; Enquist, L.W.
Science 218, 381-384, 1982
A; Title: Herpes simplex virus type-1 glycoprotein D gene: nucleotide sequence A; Reference number: A94268; MUID:83016630; PMID:6289440
A; Accession: A94268
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C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Sep-1994
C;Accession: A90945; A03729
R;Lasky, L.A.; Dowbenko, D.J.
DNA 3, 23-29, 1984
A;Title: DNA sequence analysis of the type-common glycoprotein-D genes of h A;Reference number: A90945; MUID:84131549; PMID:6321120
A;Accession: A90945
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A;Residues: 1-3,'A',5-70,'N',72-83,85-269,'R',271-282,'P',284-364,'R',366-394 <LAS>
A;Residues: 1-3,'A',5-70,'N',72-83,85-269,'R',271-282,'P',284-364,'R',366-394 <LAS>
A;Experimental source: strain Hzt
C;Superfamily: herpesvirus glycoprotein D
C;Keywords: glycoprotein; transmembrane protein
C;Keywords: glycoprotein; transmembrane protein
F;119,146,287/Binding site: carbohydrate (Asn) (covalent) #status predicted
VGBE17
glycoprotein D precursor -
C;Species: human herpesviru
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C;Superfamily: herpesvirus glycoprotein D
C;Keywords: glycoprotein; transmembrane protein
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-393/Product: glycoprotein D #status predicted <GPD>
F;341-360/Domain: transmembrane #status predicted <TMN>
F;341-360/Bomain: transmembrane #status predicted <TMN>
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C;Species: human herpesvirus 1
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C;Species: human herpesvirus 1
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A; Residues: 1-393 <LAS>
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                                                                                                                                                                                             159 QPELAPEDPEDSALLEDPV 177
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                                                                                                                                                                                                                                                                      10.5%; Score 99; DB 1; Length 394; larity 100.0%; Pred. No. 0.076; Conservative 0; Mismatches 0; Indels
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       human
us 1
                         herpesvirus
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A; Molecule type: DNA
A; Residues: 1-394 <IZU>
A; Residues: 1-394 <IZU>
A; Cross-references: GB: X54361; NID: g60414; PIDN: CAA38245.1; PID: g60415
C; Superfamily: herpesvirus glycoprotein D
C; Keywords: glycoprotein; transmembrane protein
F; 1-20/Domain: signal sequence #status predicted <SIG>F; 21-394/Product: glycoprotein D #status predicted <GPD>F; 342-360/Domain: transmembrane #status predicted <GPD>F; 342-360/Domain: transmembrane #status predicted <TMN>
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-1409 < MOU>
A; Cross-references: GB: M11240; NID: g158615; PIDN: AAA74497.1;
A; Cross-references: GB: M11240; NID: g158615; PIDN: AAA74497.1;
A; Cross-references: GB: M11240; NID: g158615; PIDN: AAA74497.1;
A; Cross-references: GB: M11240; NID: g158615; PIDN: AAA74497.1;
A; Cross-references: GB: M11240; NID: g158615; PIDN: AAA74497.1;
A; Cross-references: GB: M11240; NID: g158615; PIDN: AAA74497.1;
A; Cross-references: GB: M11240; NID: g158615; PIDN: AAA74497.1;
A; Cross-references: GB: M11240; NID: g158615; PIDN: AAA74497.1;
A; Cross-references: GB: M11240; NID: g158615; PIDN: AAA74497.1;
A; Cross-references: GB: M11240; NID: g158615; PIDN: AAA74497.1;
A; Cross-references: GB: M11240; NID: g158615; PIDN: AAA74497.1;
A; Cross-references: GB: M11240; NID: g158615; PIDN: AAA74497.1;
A; Cross-references: GB: M11240; NID: g158615; PIDN: AAA74497.1;
A; Cross-references: GB: M11240; NID: g158615; PIDN: AAA74497.1;
A; Cross-references: GB: M11240; NID: g158615; PIDN: AAA74497.1;
A; Cross-references: GB: M11240; NID: g158615; PIDN: AAA74497.1;
A; Cross-references: GB: M11240; NID: g158615; PIDN: AAA74497.1;
A; Cross-references: GB: M11240; NID: g158615; PIDN: AAA74497.1;
A; Cross-references: GB: M11240; NID: g158615; PIDN: AAA74497.1;
A; Cross-references: GB: M11240; NID: g158615; PIDN: AAA74497.1;
A; Cross-references: GB: M11240; NID: g158615; PIDN: AAA74497.1;
A; Cross-references: GB: M11240; NID: g158615; PIDN: AAA74497.1;
A; Cross-references: GB: M11240; NID: g158615; PIDN: AAA74497.1;
A; Cross-references: GB: M11240; NID: g158615; PIDN: AAA74497.1;
A; Cross-references: GB: M11240; NID: g158615; PIDN: AAA74497.1;
A; Cross-references: GB: M11240; NID: g158615; PIDN: AAA74497.1;
A; Cross-references: GB: M11240; NID: g158615; PIDN: AAA74497.1;
A; Cross-references: GB: M11240; NID: G158615; PIDN: AAA74497.1;
A; Cross-references: GB: M11240; NID: G158615; PIDN: AAA74497.1;
A; Cross-references: GB: M11240; NID: G158615; PIDN: AAA74497.1;
A; Cross-references: GB: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                copia polyprotein - fruit fly (Drosophila melanogaster) N;Contains: copia protein, 31K; copia protein, 48K; prot C;Species: Drosophila melanogaster C;Date: 04-Dec-1986 #sequence revision 04-Dec-1986 #text C;Accession: A03224; S03612; S14835
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J. Exp. Med. 172, 487-496, 1990
A;Title: Molecular and biological characterization of a herpes simplex virus type 1
A;Reference number: A47627; MUID:90324869; PMID:2165127
A;Accession: A47627
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C;Species: human herpesvirus 1
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change
C;Accession: A47627
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A;Title: Sequence determination and genetic content of the short unique region in the ger A;Reference number: A00656; MUID:85160822; PMID:2984429
A;Accession: A03730
                                                                                                                                                                                                                          A; Reference number: A03324; A; Accession: A03324
                                                                                                                                                                                                                                                                          A; Title: Complete nucleotide sequence of the Drosophila A; Reference number: A03324; MUID:85267679; PMID:2410772
                                                                                                                                                                                                                                                                                                                                                     R;Mount, S.M.; Rubin, G.M.
Mol. Cell. Biol. 5, 1630-1638, 1985
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A; Residues: 1-394 < MCG>
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C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 16-Jun-2000
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A;Residues: 1-391,1375-1409 <MIL>
A;Cross-references: EMBL:X13719; NID:g7745; PIDN:CAA31997.1; PID:g7746
A;Cross-references: EMBL:X13719; NID:g7745; PIDN:CAA31997.1; PID:g7746
R;Yoshioka, K.; Honma, H.; Zushi, M.; Kondo, S.; Togashi, S.; Miyake, T.; Shiba, T.
EMBO J. 9, 535-541, 1990
A;Title: Virus-like particle formation of Drosophila copia through autocatalytic process
A;Reference number: S14835; MUID:90151630; PMID:1689241
A;Accession: S14835
A;Molecule type: DNA
A;Residues: 1-391,1375-1409 <YOS>
A;Cross-references: EMBL:X54147; NID:g7749; PIDN:CAA38086.1; PID:g7750
C;Genetics:
glycoprotein D precursor - human
C;Species: human herpesvirus 2
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A;Cross-references: FlyBase:FBgn0000349
A;Mobile element: retrotransposon copia
C;Superfamily: retrovirus-related polyprotein
C;Keywords: polyprotein; proteinase
F;2-433/Product: copia protein, 48K #status predicted
F;2-270/Product: copia protein, 31K #status predicted
F;271-433/Product: proteinase #status predicted <MAT3>
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C;Species: human herpesvirus 2
C;Date: 03-Aug-1984 #sequence_revisic
C;Accession: A03731
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DNA 3, 23-29, 1984

A;Title: DNA sequence analysis of the type-common glycoprotein-D

A;Reference number: A90945; MUID:84131549; PMID:6321120

A;Accession: A03731
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A;Title: The nucleotide sequence of Drosophila melanogaster copia-specific 2.1-kb mRNA.
A;Reference number: S03612; MUID:89183629; PMID:2538806
A;Accession: S03612
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A; Residues: 1-393 <LAS>
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17; Conserv
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                                                                                                                                                                                                                                                      Score 91; DB 1;
Pred. No. 0.46;
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                                   (strain 333)
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                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                              Length 393;
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                                                                                                                    A; Molecule type: DNA
A; Residues: 1-313; 314-787 < YOS>
A: Cross-references: DDBJ: D10880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ş
           A;Gene: FlyBase:copia
A;Cross-references: FlyBase:FBgn0012867
A;Mobile element: retrotransposon copia
C;Superfamily: retrovirus-related polyp
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                                                                                                 C; Genetics:
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A; Molecule type: DNA
A; Residues: 1-393 <WAT>
A; Residues: 1-393 <WAT>
A; Cross-references: GB: KO1408; NID: g330268; PIDN: AAA45841.1;
C; Superfamily: herpesvirus glycoprotein D
C; Keywords: glycoprotein; transmembrane protein
F; 1-24/Domain: signal sequence #status predicted <GPD>
F; 25-393/Product: glycoprotein D #status predicted <GPD>
F; 340-356/Domain: transmembrane #status predicted <TMN>
F; 340-356/Domain: transmembrane #status predicted <TMN>
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C;Date:
C;Access
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E43674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: DNA sequence of the herpes simplex virus type 2 A;Reference number: A03732; MUID:84159516; PMID:6323270 A;Accession: A03732
                                                                                                                                                                                                          RESULT 12
PC1232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-393 < MCG>
A; Cross-references: EMBL: X04798
C; Superfamily: herpesvirus glycoprotein D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;McGeoch, D.J.; Moss, H.W.M.; McNab, D.; Frame, M.C. J. Gen. Virol. 68, 19-38, 1987
A;Title: DNA sequence and genetic content of the Hind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene 26, 307-312, 1983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R; Watson, R.J.
Gene 120, 191-196, 1992
A;Title: Efficient amplification of Drosophila simulans
A;Reference number: PC1232; MUID:93013034; PMID:1383092
A;Accession: PC1232
                                                                                        C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 C;Accession: PC1232 R;Yoshioka, K.; Kanda, H.; Takamatsu, N.; Togashi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;119,146,287/Binding site: carbohydrate (Asn) (covalent)
                                                                                                                                                         copia polyprotein - fruit fly (Drosophila simulans) retrotransposon copia (fragments) C; Species: Drosophila simulans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            utionary comparisons.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Reference number: A43674; MUID:87111457; PMID:3027242
A;Accession: E43674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;Date: 17-Mar-1987
;Accession: A03732
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Best Local
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17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 16-Jul-1999
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Pred. No. 0.46;
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                                                                                              S.; Kondo,
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                                                                                            S.; Miyake, T.; Sakaki,
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A;MOLECULE type: DNA
A;Residues: 1-1578 <GLA>
A;Cross-references: GB:AL592022; PIDN:CAC95868.1; PID:g16413076; GSPDB:GN00178
A;Experimental source: strain Clip11262
C;Genetics:
A; Olecule type: DNA
A;Residues: 1-159 <KAW>
A;Cross-references: GB:AJ248288; GB:AL096836; NID:g5458960; PIDN:CAB50612.1; PID:g545912
                                                                                                                                            R;anonymous, Genoscope submitted to the EMBL Data Library, July 1999 A;Description: Pyrococcus abyssi genome sequen A;Reference number: A75001 A;Accession: F75021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kunet, M.; Kunst, F.; Kurapkat, G.; Madueno, B.; Maitournam, A.; Macok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AD1512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: AD1512
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
                                                                                                                                                                                                                                                      ribosomal protein s18 alanine acetyltransf erase related protein PAB1226 - C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Accession: F75021
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C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Accession: AD1512
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MVAVALVFQLVPWSN1FAGAEENQTKTTQQVTQPDNQKVADENKTTV1PDNKETTKNLVN
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innocua
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29.1%; Pred. No. 11;
tive 18; Mismatches
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Pred. No. 4.6;
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Search completed: January 22, Job time: 33.6212 secs

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable N-acetylmuramoyl-L-alanine amidase [imported] - Yersinia pestis (strain C;Species: Yersinia pestis C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001 C;Accession: AD0205
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                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
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;Cross-references: GB:AL590842; PIDN:CAC90504.1; PID:g15979715; GSPDB:GN00175
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23.2%; Pred. No. 0.73;
ative 18; Mismatches 44; Indels
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Q918f3 human cytom
Q918f0 human cytom
Q918e17 human cytom
Q918e4 human cytom
Q918e6 human cytom
Q918e2 human cytom
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Q918e9 human cytom
Q918e4 human cytom
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86 GVGENLAVKAEDVEFTAGENLIWKVQIANVLELIQKLIVVKLIVINGDVVWLICVEELKVDI 143 144 TSSAYMWNMQYGMV 157 : 146 TSNAYMWNMQYGMV 159	GVGENLYVHADDVEFVPGESLKWNVRNLDVMPIFETLALRLVLQGDVIWLRCVPELRVDY	24 PDGITKAGEDALRPWKSTAKHPWFQIEDNRCYIDNGKLFARGSIVGNMSRFVFDPKADYG 83 - - : : :: :: : :	Query Match 51.6%; Score 489; DB 12; Length 203; Best Local Similarity 63.4%; Pred. No. 6.2e-41; Matches 85; Conservative 24; Mismatches 23; Indels 2; Gaps 1;	SEQUENCE 203 AA; 23262 MW; CA131FD182BE8300 CRC64;	EMBL; AF480884; AAM00783.1;	"The human cytomegalovirus genome revisited."; Submitted (FRB-2002) to the EMBL/GenBank/DDBJ databases.	, Hayward G.S., McGeoch D.J.	Davison A.J., Akter P., Dolan A., Wright K.M., Addison C.,	(+) SEQUENCE FROM N.A.	NCBI_TaxID=188763;	Betaherpesvirinae; Cytomegalovirus.	Viruses; dsDNA viruses, no RNA stage; Herpesviridae;	Chimpanzee cytomegalovirus.	(11200000000000000000000000000000000000	. 21, Last	Creat	Q8QRV5 PRELIMINARY; PRT; 203 AA.	년 1 5

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01-DEC-2001
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US3 protein.
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EMBL; AF413648; AAL14474.1; -. SEQUENCE 186 AA; 21588 MW; 3B9E8COCB54EAB70 CRC64;
                                                                                                                                                 Scott G.M., Barrell B.G., Oram J., Rawlinson W.D.;
"Characterization of transcripts from the human cytomegalovirus
TRL7, UL20a, UL36, UL65, UL94, US3 and US34.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF413650; AAL14480.1; -.
SEQUENCE 186 AA; 21558 MW; 21D1DC5ADF43DD1B CRC64;
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NCBI_TaxID=10359;
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                       NMSRFVFDPKADYGGVG-----ENLYV-----HADDVEFVPGESLKWNV-----RNL
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                                               VLVLAILAVLFLRLADSVPR----PLNVVVSEIKSAHFRVEENQCWFHMGMLYFKGRMSG
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Cytomegalovirus.
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Cytomegalovirus.
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DT US3.
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"Characterization of transcripts from the human cytomegalovirus TRI7, UL20a, UL36, UL65, UL94, US3 and US34.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF413649; AAL14477.1; -.
EMBL; AF413646; AAL14468.1; -.
EMBL; AF413647; AAL14471.1; -.
SEQUENCE 186 AA; 21556 MW; 34D58C17BE5EA06B CRC64;
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Viruses; dsDNA viruses, no RNA stag
Betaherpesvirinae; Cytomegalovirus.
MCBI_TaxID=10359;
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                                                   Scott G.M., Barrell B.G., Oram J., Rawlinson W.D.; "Characterization of transcripts from the human cytomegalovirus TRL7, UL20a, UL36, UL65, UL94, US3 and US34."; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AF413663; AAL14519.1; --
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Scott G.M., Barrell B.G., Oram
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                                                                                                                                                                  Betaherpesvirinae;
NCBI_TaxID=10359;
                                                                                                                                                                                                 Human cytomegalovirus.
Viruses; dsDNA viruses,
                                                                                                                                                                                                                                         US3 protein.
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                                         SEQUENCE
                                                                                                                          STRAIN=83A;
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                                                                                                                                           SEQUENCE FROM N.A.
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Cytomegalovirus.
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21604 MW;
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  131;
No.
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01-OCT-2002 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human cytomegalovirus.
Viruses; dsDNA viruses,
Retaherpesvirinae; Cytom
NCBI TaxID=10359;
SEQUENCE FROM N.A.
MEDLINE=22174937; PubMed=12186931;
Chang W.L., Tarantal A.F., Zhou S.S.,
"A recombinant rhesus cytomegalovirus
                                                                                                                                                                             Cercopithecine herpesvirus 8.
Viruses; dsDNA viruses, no RNA stage;
Betaherpesvirinae; Cytomegalovirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VWMLAILAVLFLRLADSVPRPLDVVV----SEIRSAHFRVEENQCWFHMGMLYFKGRMSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VFMVVYISYIYARLPDGITKAGEDALRPWKSTAKHPWFQIEDNRCYIDNGKLFARGSIVG
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Q918E2;
Q1-DEC-2001
  Human cytomegalovirus.
Viruses; dsDNA viruses, no RNA stage;
Betaherpesvirinae; Cytomegalovirus.
NCBI_TaxID=10359;
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Scott G.M., Barrell B.G., Oram J., Rawlinson W.D.;
"Characterization of transcripts from the human cytomega
"TRL7, UL20a, UL36, UL65, UL94, US3 and US34.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF413665; AAL14524.1; -.
SEQUENCE 186 AA; 21602 MW; 3BE0504768183511 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human cytomegalovirus.
Viruses, dsDNA viruses, no RNA stage,
Betaherpesvirinae, Cytomegalovirus.
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J. Virol. 76:9493-9504(2002).
EMBL; AF474179; AAM97606.1; -.
SEQUENCE 196 AA; 23115 MW;
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EMBL; AF413651; AAL14483.1; -. SEQUENCE 186 AA; 21533 MW; CREONITED
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Q910G4;
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01-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human cytomegalovirus.
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Cytomegalovirus.
NCBI_TaxID=10363, 10359;
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EMBL; AY038933; AAK71882.1; -.
SEQUENCE 186 AA; 21515 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPECIES=Human cytomegalovirus (strain Towne); STRA Liu W., Zhao Y., Biegalke B.J.; "Analysis of human cytomegalovirus US3 proteins."; Submitted (JUN-2001) to the EMBL/GenBank/DDBJ data
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                                                                              FETLALRLVLQGD-VIWLRCVPELRVDYTSSAYMWNMQ 153
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                                 --TLSTR---WGDPKKYAACVPQVRMDYSSQTINWYLQ
                                                                                                                                                                                      NMSR-----FVFDPKADYGGVGENLYVHADDVEFVPGESLKWNV-----RNLDVMPI
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RESULT 11
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OC Betal
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01-MAR-2002
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Scott G.M., Barrell B.G., Oram J., Rawlinson W.D.;
Scott G.M., Barrell B.G., Oram J., Rawlinson W.D.;
"Characterization of transcripts from the human cytomegalovirus
"Characterization of transcripts from the human cytomegalovirus
TRL7, UL20a, UL36, UL65, UL94, US3 and US34.";
TRL7, UL20a, UL36, UL65, UL94, US3 and US34.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF413648; AAL14475.1; -.
EMBL; AF413648; AAL14475.1; -.
EMBL; AF413648; AAL14475.1; -.
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Viruses; dsDNA viruses, no RNA stage
Betaherpesvirinae; Cytomegalovirus.
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Viruses; dsDNA viruses,
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NMSRFVFDPKADYGGVG-----ENLYV-----HADDVEFVPGESLKWNV------RNL
                                                      VLMLAILAVLFLRLADSVPR----PLNVVVSEIKSAHFRVEENQCWFHMGMLYFKGRMSG
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2; Mismatches 6
                                                                                                                                                        Score 112.5; DB 
Pred. No. 0.0021; 
2; Mismatches 4
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Query Match 11.5%; Sometime Sent Local Similarity 24.9%; Particles 42; Conservative 33;
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                                                                                                                                     SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=17A, 47A, and 48A;

STRAIN=17A, 47A, and 48A;

Scott G.M., Barrell B.G., Oram J., Rawlinson W.D.;

"Characterization of transcripts from the human cytomegalovirus TRL7, UL20a, UL36, UL94, US3 and US34.";

Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AF413649; AAL14478.1; -.

EMBL; AF413646; AAL14470.1; -.

EMBL; AF413647; AAL14472.1; -.

EMBL; AF413647; AAL14472.1; -.

SEQUENCE 149 AA; 17185 MW; 1888394AC2DF553C CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
1mmediate-early glycoprotein US3.
Chimpanzee cytomegalovirus.
Viruses; dsDNA viruses, no RNA stage; Herpesviridae
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NCBI_TaxID=188763;
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Score 108.5; DB 12;
Pred. No. 0.0052;
3; Mismatches 49;
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Q1-DEC-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
                                                                                                                                                                                                                                                                                            Scott G.M., Barrell B.G., Oram J., Rawlinson W.D.;
Scott G.M., Barrell B.G., Oram J., Rawlinson W.D.;
"Characterization of transcripts from the human cytomegalovirus
"RL7, UL20a, UL36, UL65, UL94, US3 and US34.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF413650; AAL14481.1; -.
SEQUENCE 149 AA; 17201 MW; 0523494C741B3A79 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viruses; dsDNA viruses, no RNA stage; Betaherpesvirinae; Cytomegalovirus.
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KAD_STRMU
GHD_CHLTE
ATFYS_SCHPO
RNG_ECOLI
CDGT_BACCS
SYV_MCTJVA
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SYV_MCTJVA
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GPHI_PSEAE
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P31746 bacillus sp
P39832 escherichia
P04146 drosophila
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EMBL; X04650; CAB37097.1; -.
EMBL; M18921; AAA45958.1; -.
PIR; F26078; QQBEC6.
Early protein; Glycoprotein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Chee M.S., Bankier A.T., Beck S., Bohni R., Brown C.M., Cerny R., Horsnell T., Hutchison C.A. III, Kouzarides T., Martignetti J.A., Preddie E., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B. "Analysis of the protein-coding content of the sequence of human cytomegalovirus strain AD169.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human cytomegalovirus (strain AD169).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Cytomegalovirus.
NCBI_TaxID=10360;
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01-MAR-1989 (Rel. 10, Last sequence update)
01-FEB-1991 (Rel. 17, Last annotation updat
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"Sequence of the short unique region, short repeats, and long repeats of human cytomegalovirus.";
J. Mol. Biol. 192:177-208(1986).
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                            FVPGESLKWNV-----RNLDVMPIFETLALRLVLQGD-VIWLRCVPELRVDYTS
                                                           FRVEENQCWFHMGMLYFKGRMSGNFTEKHF---VNVGIVSQSYMDRLQVSGEQYHHDE--
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InterPro; IPR006589; Alp_amyl_cat_sub.
InterPro; IPR006048; Alpha_amyl_C.
InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR002044; CBD 4.

InterPro; IPR006046; Glyco_hydro_13.
InterPro; IPR002909; IPT TIG.
Pfam; PF00128; alpha-amylase; 1.
Pfam; PF02806; alpha-amylase_C; 1.
Pfam; PF02806; CBM_20; 1.
Pfam; PF01833; TIG; 1.
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01-JUL-1993 (Rel. 26, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Cyclomaltodextrin glucanotransferase precursor
(Cyclodextrin-glycosyltransferase) (CGTase).
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Proceedings of the fourth international symposium pp.71-76, Kluwer Academic Publishers, Dordrecht an -!- CATALYTIC ACTIVITY: Degrades stand
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"Cloning and nucleotide sequence of a cyclodextrin glycosyltransferase gene from the alkalophilic Bacillus 1-1.";
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Bacteria; Firmicutes; Bacillales; Bacillaceae;
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ProDom; PD001568; CBD_4; 1.
SMART; SM00642; Aamy; 1.
SMART; SM00632; Aamy_C; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MISCELLANEOUS: CGTASE MAY CONSIST OF TWO PROTEIN DOMAINS: THE ONI IN THE AMINO-TERMINAL SIDE CLEAVES THE ALPHA-1,4-GLUCOSIDIC BOND IN STARCH, AND THE OTHER IN THE C-TERMINAL SIDE CATALYZES OTHER ACTIVITIES, INCLUDING THE RECONSTITUTION OF AN ALPHA-1,4-GLUCOSIDIC LINKAGE FOR CYCLIZING THE MALTOOLIGOSACCHARIDE PRODUCED.

SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATALYTIC ACTIVITY: Degrades starch of a 1,4-alpha-D-glucosidic bond. COFACTOR: BINDS TWO CALCIUM IONS.
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                                                                                                                         12 TAKHPWFQIEDNRCYIDNGKLFARGSIVGNMSRFVFDPKADYGGVGENLYVHADDVEFVP
     72
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  GE-SLKWNVRNLDVMPIFETLALRLVLQGDVIWL-RCVPELRVD
                                                                   TPNHSSPALETNPNYVENGAIYDNGALLGN-----YSNDQQNLFHHNGGTDFSS 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
SETRAIN=K12 / MG1655;

STRAIN=K12 / MG1655;

MEDLINE=97426617; PubMed=9278503;

Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;

"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                                                                                                                                                                                           Patzer S.I., Hantke K.;
"The ZnuABC high-affinity zinc uptake system and its regulator Zur Escherichia coli.";
Mol. Microbiol. 28:1199-1210(1998).
-!- FUNCTION: INVOLVED IN THE HIGH-AFFINITY ZINC UPTAKE TRANSPORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 80-261 FROM N.A.
MEDLINE=88314937; PubMed=2842314;
Shinagawa H., Makino K., Amemura M., Kimura S., Iwasaki H., Nakata A.;
"Structure and regulation of the Escherichia coli ruv operon involved in DNA repair and recombination.";
J. Bacteriol. 170:4322-4329(1988).
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Escherichia.
                                         TO THE ABC-3 SUBFAMILY OF INTEGRAL OH.INFLUENZAE ZNUB.
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               "The nucleotide sequence of Drosophila 2.1-kb mRNA.";
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EMBL; D90828; BAA15667.1; -.
EMBL; D90829; BAA15670.1; -.
EMBL; U38702; AAA81031.1; -.
EMBL; M21298; -; NOT ANNOTATED CDS.
                                                                   SEQUENCE FROM N.A. (ISOFORM SHORT MEDLINE=89183629; PubMed=2538806; Miller K., Rosenbaum J., Zbrzezna
                                                                                                                                                            MEDLINE-85240569; PubMed=2409449;
Emori Y., Shiba T., Kanaya S., Inou
"The nucleotide sequences of copia
virus-like particles.";
Nature 315:773-776(1985).
                                                                                                                                                                                                                                                                                                    Mount S.M., Rubin G.M.;
Mount S.M., Rubin G.M.;
Mount S.M., Rubin G.M.;
Moont S.M., Rubin G.M.;
Moont S.M., Rubin G.M.;
Rubin G.M.;
Molation Representation of the Drosophila transposable element copia; homology between copia and retroviral proteins.";
Mol. Cell. Biol. 5:1630-1638(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COPI DROME STANDARD; PRT; 1409 AA.

P04146; Q03728; Q24280; Q24555; Q24585; Q24586; Q24587;
01-NOV-1986 (Rel. 03, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Copia protein [Contains: Copia VLP protein; Copia protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoā; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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   Acids Res. 17:2134-2134(1989)
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SMART; SM00343; ZnF C2HC; 1.

PROSITE; PS00141; ASP PROTEASE; FALSE_NEG.

PROSITE; PS50158; ZF_CCHC; 1.

Transposable element; Hydrolase; Aspartyl protease; ATP-binding; Polyprotein; Alternative splicing; Polymorphism; Zinc-finger.

Polyprotein; Alternative splicing; Polymorphism; Zinc-finger.

COPIA VLP PROTEIN (POTENTIAL).

COPIA PROTEASE (POTENTIAL).

TAMOS

COPIA PROTEASE (POTENTIAL).
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MEROPS; All.001; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001969; Aspprotease_site.
InterPro; IPR001584; Rve.
InterPro; IPR001878; Znf_CCHC.
Pfam; PF00665; rve; 1.
Pfam; PF00098; zf-CCHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shiba T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=90151630; PubMed=1689241; Yoshioka K., Honma H., Zushi M.,
                                                                                                                                                                                                                                                                                            VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Virus-like particle formation of Drosophila copia through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FlyBase; FBgn0013437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IBOId=P04146-2; Sequence=VSP_005226; SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE SIMILARITY: Contains 1 CCHC-type zinc finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=Short;
                                                            1048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Event=Alternative splicing; Named isoforms=2;
                             72
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                                                                                                                      24;
                                                                                                                                      Similarity
                             GESLKWN------VRNLDVMPIFETLALRLVLQGDVIWL 104
                                                            WFEVFEQALKECEFVN
                                                                                        WFQIED---NRCYIDNGKLFARGSIVGNMSRFVFDPKADYGGVGENLYV--HADDVEFVP 71
GDMTRMNNFKRYLMEKFRMTDLNEIKHFIGIRIEMQEDKIYL 1137
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23.5%;
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                                                                                                                                                             SFVGIQRDRTQ (IN VARIANT COPIA-RELATED).
MISSING (IN VARIANT COPIA-RELATED).
D->A: LOSS OF ACTIVITY.
S -> N (IN REF. 2; CAA26447).
I -> V (IN REF. 2; CAA26447).
Q -> E (IN REF. 2; CAA26447).
Q -> E (IN REF. 2; CAA26447).
                                                                                                                     18;
                                                                                                                                      Score 72; DB 1;
Pred. No. 13;
                                                                                                                                                                                                                                                                           STTGYLFKMFDFNLICWNTKRONS -> VQQGIYSKCLILI
SFVGIQRDRTQ (IN VARIANT COPIA-RELATED).
                                                                                                                                                                                                                                                                                                           CCHC-TYPE.
PROTEASE (BY SIMILARITY).
Missing (in isoform Short).
/FTId=VSP_005226.
                                                                                                                        Mismatches
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                                                          -SSVDRCIY--ILDKGNINENIYVLLYVDDVVIAT 1095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TO PEPTIDASE FAMILY A11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Togashi S., Miyake
                                                                                                                     34;
                                                                                                                                                  Length 1409;
                                                                                                                        Indels
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                                                                                                                     Gaps
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RESULT 6
CDGT_BACOH
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InterPro; IPR006048; Alpha_amyl_C.
InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR002044; CBD_4.
InterPro; IPR006046; Glyco_hydro_13.
InterPro; IPR002909; IPT_TIG.
Pfam; PF00128; alpha-amylase; 1.
Pfam; PF02806; alpha-amylase_C; 1.
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01-AUG-1992 (Rel. 2
01-NOV-1995 (Rel. 3
01-NOV-1995 (Rel. 3
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DISULFID
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Appl. Microbiol. Biotechnol. 35:600-605(1991).
-I- CATALYTIC ACTIVITY: Degrades starch to cyclodextrins by formation of a 1,4-alpha-D-glucosidic bond.
-I- COPACTOR: BINDS TWO CALCIUM IONS.
                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00110; ALPHAAMYLASE.
ProDom; PD001568; CBD_4; 1.
SMART; SM00642; Aamy; 1.
SMART; SM00632; Aamy_C; 1.
Transferase; Glycosyltransferase; Calcium; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE=92000599; PubMed=1368710;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus ohbensis.
Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1992 (Rel. 23, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Cyclomaltodextrin glucanotransferase precursor (Cyclodextrin-glycosyltransferase) (CGTase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDGT_BACOH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF02806; alpha-an Pfam; PF00686; CBM_20; Pfam; PF01833; TIG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; D90243; BAA14289.2; -. HSSP; P31797; 1CYG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http:\bar{/}/www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
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SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: Monomer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KNOWN AS THE ALPHA-AMYLASE FAMILY.
12 TAKHPWFQIEDNRCYIDNGKLFARGSIVGNMSRFVFDPKADYGGVGENLYVHADDVEFVP
                                                     26;
                                                                              Similarity
                                                                                                                                                             704 AA;
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68
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                                                       Conservative
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25.0%;
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                                                       21;
                                                     Score 70.5; D
Pred. No. 8.7;
21; Mismatches
                                                                                                                                                         CYCLOMALTODEXTRIN GLUCANOTRANSFERASE.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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; 04FA14951D5ACECB CRC64;
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RESULT 7
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CARBOHYD 75 75 1

CARBOHYD 98 98 1

CARBOHYD 140 140 1

SEQUENCE 349 AA; 39114 MW;
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PIR; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Analysis of the protein-coding content of the sequence cytomegalovirus strain ADI69.";
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Chee M.S., Bankier A.T., Beck S., Bohni R., Brown C.M., Cerny R.,
Horsnell T., Hutchison C.A. III, Kouzarides T., Martignetti J.A.,
Preddie E., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [2]
COMPLETE GENOME
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NCBI_TaxID=10360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-FEB-1991 (Rel. 17, Last annotation updat
Hypothetical protein HHRF5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Curr. Top. Microbiol. Immunol. 154:125-169(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Juman cytomegalovirus (strain AD169).
Jiruses; dsDNA viruses, no RNA stage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E27216; QQBED5.
                                                                           201
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                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                             QCRLRNGATFSKGDIEGNFSGPVVVELDYEDIDITGERQRLRFHLSGLGCPTKENIRKDN 140
                                                                         GKNAEVPPATRTSSTYSVLSAFVVWI 226
                                                                                                                                                                             ESDVNGGIRWALYIQTGDAKYGIRNQHLSIRLMYPGEKNTQQLLDSDFSCERHRRPSTPL 200
                                                                                                                                                                                                                              KADY-GGVGENLYVHADDVEF-------VPGESLKWNV-----
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Pred. No. 4.9;
L6; Mismatches
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Best Local
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promoter.";
Mol. Microbiol. 16:1099-1109(1995).
-!- CATALYTIC ACTIVITY: UDP-glucose + alpha-D-ga
alpha-D-glucose 1-phosphate + UDP-galactose.
                                                                                                                                                                                                                          01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Galactose-1-phosphate uridylyltransferase (EC 2.7.7.12)
uridylyltransferase) (UDP-glucose--hexose-1-phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Mao Y., Xie Y., Jiang M.;

"cDNA cloning of a novel human F-box protein.";

"cDNA cloning of a novel human F-box protein.";

Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: Probably recognizes and binds to some phosphorylated proteins and promotes their ubiquitination and degradation.

-i- SUBUNIT: PART OF A SCF (SKP1-CULLIN-F-BOX) PROTEIN LIGASE COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FX16_HUMAN
Q8IX29;
15-SEP-2003
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SMART; SM00256; FBOX; 1.
PROSITE; PS50181; FBOX; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                    SEQUENCE FROM N.A.
MEDLINE=96020643; PubMed=8577246;
Wickes B.L., Edman J.C.;
                                                                                                                                                           Cryptococcus neoformans (Filobasidiella neoformans). Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Hete Tremellomycetidae; Tremellales; Tremellaceae; Filoba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HUMAN
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-!- SIMILARITY: Contains 1 F-box domain.
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                                                                      "The Cryptococcus
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L5-SEP-2003 (Rel.
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Pred. No. 4.5;
4; Mismatches
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                                                                                                                                                             ; Hymenomycetes; Heterobasidiomycetes; Tremellaceae; Filobasidiella.
                                                                       gene
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InterPro; IPR005851; Galp_Utransf_1.
InterPro; IPR005850; Galp_Utransf_C.
InterPro; IPR005849; Galp_Utransf_N.
Pfam; PF02744; Galp_UDp_tr_C; 1.
Pfam; PF01087; Galp_UDp_transf; 1.
ProDom; PD005051; Galp_UDptransf1; 1.
TISSUE=Blood;
MEDLINE=97271556; PubMed=9126482;
YOShiyama K., Higuchi Y., Kataoka M., Matsuura K., Yamamoto S.;
YOShiyama ADAM8): expression, primary amino acid sequence, and
gene location.";
Genomics 41:56-62(1997).
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SEQUENCE
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P78325;

01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
ADAM 8 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase domain 8) (Cell surface antigen MS2) (CD156a antigen) (CD156).

ADAM8 OR MS2.

Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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PROSITE; PS00117; GAL_P_UI
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(See http://www.isb-sib.ch/announce/
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                                                                                          Query Match
Best Local S
Matches 29
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InterPro; IPR001762; Disintegrin.
InterPro; IPR006209; EGF like.
InterPro; IPR006210; IEGF.
InterPro; IPR002870; Pep_M12B_propep.
InterPro; IPR001590; Reprolysin.
InterPro; IPR001590; Zn_MTpeptdse.
                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS5021:
PROSITE; PS0042:
PROSITE; PS5021:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- FUNCTION: POSSIBLE INVOLVEMENT IN EXTRAVASATION OF LEUKOCYTES.
-!- COFACTOR: Binds 1 zinc ion per subunit (Probable).
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- TISSUE SPECIFICITY: EXPRESSED ON NEUTROPHILS AND MONOCYTES.
-!- SIMILARITY: Belongs to peptidase family M12B.
-!- SIMILARITY: Contains 1 disintegrin domain.
-!- SIMILARITY: Contains 1 disintegrin domain.
-!- DATABASE: NAME-PROW; NOTE-CD guide CD156 entry;
www-"http://www.ncbi.nlm.nih.gov/prow/cd/cd156.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
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SMART; SM00050; DISIN; 1.
SMART; SM00181; EGF; 1.
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Pfam; PF01421; Reprolysin; 1.
PRINTS; PR00289; DISINTEGRIN.
ProDom; PD000664; Disintegrin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEROPS; M12.208; -.
Genew; HGNC:215; ADAM8.
MIM; 602267; -.
GO; GO:0005888; C:proteoglycan integral to
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                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS01186; PROSITE; PS00142;
                                                                                                                                                                                                                               METAL
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                                                                                                                                                                                                                                                                                                                                                                            Transmembrane;
                                        151
              60
                                                                                                                                                                                                                                                                                                                                                                                                  3; PS50215; ADAM MEPRO; 1.
3; PS00427; DISINTEGRIN_1; I
3; PS50214; DISINTEGRIN_2; I
3; PS501186; EGF 2; UNKNOWN I
3; PS01186; EGF 2; UNKNOWN I
                                                                                             29;
                                                                                                         Similarity
-LYVHADDVEF-VPGESLKWNVRNLDVM----PIFETLALRLVLQGDVIW 103
                                       RHAVYQAEHLLQTAGTCGVSDDSL---GSLLGPRTAAVFRPRP-----GDSLPSRETRYV
                                                                  KHPWFQIED-----NRCYIDNGKLFARGSIVGNMSRFVFDPKADYGGVGEN---
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                                                                                          10.7%; ilarity 26.4%; Conservative 18
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28-FEB-2003 (Rel. 41, L
28-FEB-2003 (Rel. 41, L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 413:852-856(2001).

-!- FUNCTION: TRANSPORT PROTEIN FOR SUGAR PHOSPHATE UPTAKE.

-!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane

-!- INDUCTION: EXTERNAL GLUCOSE-6-PHOSPHATE INDUCES THE EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE008876; AAL22645.1; -. PIR; D41853; D41853. StyGene; SG10409; uhpT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=92234930; PubMed=1569007; Island M.D., Wei B.-Y., Kadner R.J.; "Structure and function of the uhp genes transport system in Escherichia coli and J. Bacteriol. 174:2754-2762(1992).
                                                                                                                                                                                                                                                                                                         StyGene; SG10409; uhpT.
InterPro; IPR000849; GlpT_transporter.
InterPro; IPR007114; MFS.
InterPro; IPR005828; Sub_transporter.
Pfam; PF00083; sugar_tr; 1.
TIGRFAMS; TIGR00881; 2A0104; 1.
PROSITE; PS00942; GLPT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M89480; AAA27246.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Salmonella typhimurium
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                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE SLC37A FAMILY OF TRANSPORTERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OF THE UHP-REGION
                                                                                                                                                                                                                                                             lete
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t; Sugar transport;
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                                             (PROBABLE)
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RESULT 12
ATC7_YEAST
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A Chillingworth T., Connor R., Devlin K., Gentles S., Hamlin N.,
A Harris D.E., Horsnell T., Hunt S., Jagels K., Jones M., Lye G.,
A Moule S., Odell C., Pearson D., Rajandream M.A., Rice P., Rowle
A Moule S., Smith V., Walsh S., Whitehead S., Barrell B.G.;
"The nucleotide sequence of Saccharomyces cerevisiae chromosome
L Nature 387:84-87(1997).
C -!- FUNCTION: THIS MAGNESIUM DEPENDENT ENZYME CATALYZES THE HYI
OF ATP COUPLED WITH THE TRANSPORT OF PHOSPHOLIPIDS (POTENTI
C LEADS TO NEOMYCIN-RESISTANCE WHEN OVEREXPRESSED.
C -!- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + phosphate.
C -!- SUBCELLULAR LOCATION: Integral membrane protein.
C -!- SIMILARITY: Belongs to the cation transport ATPases family
C ATPases). Subfamily IV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YEAST
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P40527;
01-FEB-1995
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CONFLICT
CONFLICT
SEQUENCE
                                              This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
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DOMAIN
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TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Potential phospholipid-transporting ATPase 4 (EC
                       entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                     PubMed=9169870;
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=4932;
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250 274
275 294
295 318
19 327
28 344
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1 379
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P -> A (IN REF.
GA -> AL (IN REF.
G -> A (IN REF.
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Pred. No. 14;
7; Mismatches
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CYTOPLASMIC
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C13398B21CEA92DA CRC64;
                                    noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                             Jones M., Lye G.,
A. Rice P., Rowley N.,
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                                                                                                                                                                                                                                                                                          Brown D.,
Hamlin N.,
                                                                                                                                            family (P-type
                                                                                                                                                                                                  THE HYDROLYSIS (POTENTIAL).
                                                                                         a collaboration
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EMBL; Z38060; CAA86174.1;

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Best Local :
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Q8DS33;
15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Adenylate kinase (EC 2.7.4.3) (ATP-AMP transphosphorylase).
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TIGRFAMS; TIGR01652; ATPASE-Plipid;
TIGRFAMS; TIGR01494; ATPASE-P-type;
PROSITE; PS00154; ATPASE-E1-E2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001757; ATPase_E1-
InterPro; IPR006539; Flippase.
InterPro; IPR005834; Hydrolase.
InterPro; IPR005834; Hydrolase; 1-
Pfam; PF00122; E1-E2 ATPase; 1.
Pfam; PF00702; Hydrolase; 1.
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SGD;
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                                                                                                                                                     STRAIN=UA159 / ATCC 700610 / Serotype C;
MEDLINE=22295063; PubMed=12397186;
Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S., Qian
Li S., Zhu H., Najar F., Lai H., White J., Roe B.A., Ferretti J.J.;
"Genome sequence of Streptococcus mutans UA159, a cariogenic dental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
                                                                                                                                                                                                                                                                           Streptococcus mutans.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                  Proc.
                                                                                                                                           pathogen.
                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                     ADK OR SMU.2005
                                                                                                                                                                                                                                                    NCBI_TaxID=1309;
                                                          SUBUNIT: Monomer (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: Belongs to the adenylate kinase family.
                                                                                             FUNCTION: This small ubiquitous enzyme is maintenance and cell growth.

CATALYTIC ACTIVITY: ATP + AMP = ADP + ADP.
            veen the Swiss Institute of Bioinformatics Institute
                                                                                                                      :. Natl. Acad. Sci. U.S.A. FUNCTION: This small ubiqu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S48431; S48431.
S0001310; NEO1.
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   non-profit
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1110
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417
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210
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Pred.
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POTENTIAL.
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PHOSPHORYLATION (PROBABLE).
W; DC7225CC9577DBE6 CRC64;
                                                                                                                       99:14434-14439(2002).
uitous enzyme is essential
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    There are no restrictions 
ng as its content is in
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RESULT 14
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Best Local (
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InterPro; IPRO01637; GLN_synth.
InterPro; IPRO01637; GlnA_adenyltr
Pfam; PF00120; gln-synt; 1.
Pfam; PF03951; gln-synt_N; 1.
ProDom; PD001057; Gln_synt_C; 1.
PROSITE; PS00180; GLNA_1; 1.
PROSITE; PS00181; GLNA_ATP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
01-OCT-1993 (Rel. 27, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Glutamine synthetase (EC 6.3.1.2) (Glutamate--ammonia ligase).
Panulirus argus (Spiny lobster).
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Palinura;
Palinuroidea; Palinuridae; Panulirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGREAMS; TIGR01351; adk; 1.

PROSITE; PS00113; ADENYLATE KINASE; 1.

Transferase; Kinase; ATP-binding; Complete proteome.

NP BIND 7 15 ATP (BY SIMILARITY).

SEQUENCE 212 AA; 23638 MW; 5AF9C1AD9B5D5520 CRC6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE015024; AAN59609.1; -. HAMAP; MF_00235; -; 1. Pfam; PF00406; ADK; 1. ProDom; PD000657; Adenylate_ki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                       "cDNA clones from the olfactory organ of the spiny protein related to eukaryotic glutamine synthetase. Gene 129:275-278(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PANAR
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                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Olfactory organ;
MEDLINE=93314973; PubMed=8100791;
Trapido-Rosenthal H.G., Linser P.J.,
Carr W.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLNA PANAR
Q04831;
                                                                                                           EMBL; M96798; AAA02583.1; -. PIR; JN0716; JN0716. HSSP; P06201; ILGR.
                                                                                                                                                                                   use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-
                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                       -i- CATALYTIC ACTIVITY:
                                                                                                                                                                                                                                                                                               L-glutamine.
SUBUNIT: Homooctamer.
SUBCELLULAR LOCATION:
SIMILARITY: BELONGS TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              173
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23.7%;
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Ladenyltn.
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O THE GLUTAMINE SYNTHETASE FAMILY
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Pred. No. 6.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                         moved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                             + NH(3) = ADP +
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
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SEQUENCE
                                                                                                                                                                                                                                                                                                          Eisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,
Dodson R.J., Deboy R., Gwinn M.L., Nelson W.C., Haft D.H.,
Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.L., Yang F.,
Holt I., Umayam L.A., Mason T., Brenner M., Shea T.P., Parksey D.,
Nierman W.C., Feldblyum T.V., Hansen C.L., Craven M.B., Radune D.,
Vamathevan J., Khouri H., White O., Gruber T.M., Ketchum K.A.,
Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.;
"The complete genome sequence of Chlorobium tepidum TLS, a
photosynthetic, anaerobic, green-sulfur bacterium.";
Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514(2002).
-!- FUNCTION: Involved in bacteriochlorophyll biosynthesis; introduces
a magnesium ion into protoporphyrin IX to yield Mg-protoporphyrin
                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

MEDLINE=20433268; PubMed=10976061;

Xiong J., Fischer W.M., Inoue K., Nakahara M., Bauer C.E.;

"Molecular evidence for the early evolution of photosynthesis.";

Science 289:1724-1730(2000).
                    EMBL; AY005135; AAG12406.1; -.
EMBL; AE012889; AAM72526.1; -.
TIGR; CT1296; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=TLS / ATCC 49652 / DSM 12025; MEDLINE=22103685; PubMed=12093901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Chlorobi, Chlorobia; Chlorobiales; Chlorobiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chlorobium tepidum.
                                                                                           or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                        PATHWAY: Bacteriochlorophyll biosynthesis. SIMILARITY: BELONGS TO THE MG-CHELATASE SUBUNITS D/I FAMILY. SIMILARITY: Contains 1 WWFA domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGVGANRVYGRDVVEAHYRACLCAGINISGENAK-----VMPAQWEFQVGPCEGITMG
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IPR000523; Mg_chelatse_chII.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.5%; Score 66; DB 1; Length 361
23.2%; Pred. No. 12;
tive 14; Mismatches 44; Indels
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Best Local
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                                                                                                                                                                                                       InterPro; IPR002035; VWF A.

Pfam; PF01078; Mg_chelatase; 1.

Pfam; PF00092; vwa; 1.

PROSITE; PS50234; VWFA; 1.

Photosynthesis; Bacteriochlorophyll biosynthesis; Complete proteome.

DOMAIN 277 329 GLU/PRO-RICH.
                                                                                                                                                                               SEQUENCE
455 VASLLQNAYVHRDQVSLISFRGKQAQVLLPPSQSVDRAKRELDVLP 500
                                                         401 EQAKKGIKSTAALIIGKD---DIKIKRFRDKSGTLFIFMVDASGSMALNRMR---QAKGA 454
                            5
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                                                                                                                                    Similarity
                                                                              EDALRPWKSTA----KHPWFQIEDNRCYIDNGKLF----ARGSIVGNMSRFVFDPKAD 52
                           YGGVGENLYVHADDVEFV-----PGESLKWNVRNLDVMP 86
                                                                                                                                                                             432
620 AA;
                                                                                                                    Conservative
                                                                                                                                                                                              620
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                                                                                                                   10.5%; Score 66; DB 1; Length 620; 29.2%; Pred. No. 23; Live 10; Mismatches 37; Indels
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Search completed: January 22, 2004, 11:39:40 Job time: 19.4198 secs

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Gapop 10.0 , Gapext 0.5
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1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*

2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*

3: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*

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Cytomegalovirus US
Cytomegalovirus US
Hydrophobic protei
Hydrophobic protei
Glutathione-S-tran
Human VEGF-X prote
Human VEGF-X prote
Infectious salmon
Muscarinic acetylc
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Secretion signal a	AAW85766	20	26	9.2	87.5	ί'n
Targeting molecule	AAW61590	19	26	9.2	87.5	4
	AAW64613	19	26	9.2	87.5	بنا
ਜ	AAW72013	19	400	9.6	91	ັນ
SB5	AAW72143	19	400	9.6	91	ï
n.	AAP50581	σ	394	9.6	91	Ö
ூ	AAW72163	19	393	9.6	91	Ö
2	AAW11324	18	393	9.6	91	œ
Herpes Simplex vir	AAP90748	10	393	9.6	. 91	7
Sequence of Herpes	AAP40084	Ç	393	9.6	91	ō
HSV antigen gD2.	AAW12068	16	368	9.6	91	ັກ
Honey bee melittin	AAW87499	20	21	10.2	97	4
Honey bee melittin	AAR99533	17	21	10.2	97	ũ
m.	ABG31288	23	20	10.2	97	Ñ
Honeybee melittin	AAM52506	23	21	10.3	98	ŭ
HSV-1 US6-associat	AAM49704	23	509	10.5	99	Ö
Sequence encoded b	AAP50582	σ	394	10.5	99	Ö
Sequence of Herpes	AAP40083	თ	394	10.5	99	œ
Herpes Simplex vir	AAP90887	10	393	10.5	99	7
HSV glycoprotein D	AAW11323	18	388	10.5	99	ð
HSV gD1 peptide fr	AAW81601	20	369	10.5	99	ហ៊
Polypeptide with a	AAR06489	片	369	10.5	99	4.
HSV glycoprotein D	AAW11322	18	308	10.5	99	ũ
HSV-1 US6-associat	AAM49703	23	124	10.5	99	Ñ
Recombinant vaccin	AAY70278	22	350	10.8	102	ï
Baculovirus expres	ABG74777	24	129	10.8	102	Ö
Human GIL-19/AE289	AAB36293	21	49	10.8	102	ø
6His affinity tag	ABB79912	23	48	10.8	102	œ
Honey bee melittin	AAY70301	21	22	10.8	102	7
Melittin protein s	ABU08142	24	21	10.8	102	g
Honeybee melittin	AAM52328	23	21	10.8	102	ij
Honeybee melittin	AAU76918	23	21	•	102	4.
Honeybee melittin	ABB10034	23	21	•	102	w
Heterologous signa	ABG31292	23	21	10.8	102	N
Melittin signal pe	AAB72437	22	21	10.8	102	1
Signal peptide of	AAG63690	22	21	10.8	102	0

ALIGNMENTS

RESULT 1 AAY97249

AAY97249;

DEC-2000

(Pirst entry)

AAY97249 standard; Protein; 177

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US2; hCMV; major histocompatibility complex; MHC; class I; clast antigen presentation; inhibition; CD8-positive; CD4-positive; transplant; gene therapy; immunosuppressive; fusion; DL6.
                                                                                                          Key
                                                                                                                                             Chimeric - Human cytomegalovirus.
Chimeric - Apis sp.
10-AUG-2000.
                                           Peptide
                                                             Misc-difference
                                                                                Protein
                                                                                                                            Chimeric
                                                                                                                                     Chimeric
                                                                                                                                                                                                             Cytomegalovirus US2t-DL6 fusion protein.
                WO200046361-A1.
                                                                                                Peptide
                                                                                                                             1 1
                                                                                                                            Apis sp.Homo sapiens.Synthetic.
                                                                                                         Location/Qualifiers
                                                                                /label= Bee_mellitin_signal_peptide
22...157
                                 /label= DL6_epitope
                                            note= "Single glycine spacer"
|59..177
                                                                    label= Soluble_US2_protein
                                                                                                                                                                                  cell;
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RESULT 2
AAY97248
ID AAY9
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DT 04-I
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Matches 177
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                                                                                         Human cytomegalovirus
                                                                                                                                                                                                                         US2; hCMV; major histocompatibility complex; MHC; class I; class antigen presentation; inhibition; CD8-positive; CD4-positive; T of the complex is the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the compl
                                                                                                                                                                                                                                                                                                                                                             Cytomegalovirus US2 protein
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       WO200046361-A1
                                                                                                                                                                              antigen presentation;
transplant; gene thera
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard; Protein; 199 AA.
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                                                                                                                                                                              gene therapy; immunosuppressive.
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100.0%; Pred.
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No. 7.9e-99;
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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 136; Conserv
                transmembrane protein; monotopic membrane protein; polytopic membrane protein; pump; channel; receptor kinase; g protein-coupled receptor; transporter protein.
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                                                                Signal sequence; ligand identification; hydrophobic protein.
                                                                                                Hydrophobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inhibiting recognition of cellular tissue by CD8+ and CD4+ T cells, treat or prevent autoimmune diseases, and to improve gene therapy, comprises introducing human cytomegalovirus US2 protein into cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB;
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                                                                                                                                  21-OCT-2002
                                                                                                                                                                                                ABG31298 standard;
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DB; AAA53813.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           199 AA;
                                                                                               protein mellitin tag tag-Human beta2-adrenergic receptor
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                                                                                                                                                                                                 Protein;
                                                                                                                                  entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78.1%; Score 740; DB 21; 100.0%; Pred. No. 2.5e-75; tive 0; .Mismatches 0;
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                                                                                                                                                                                                                  RESULT
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      membrane, integral membrane, transmembrane, monotopic or polytopic membrane, pump, channel, receptor kinase, G protein-coupled receptor, or transporter protein, or membrane-associated enzyme, or Myc tag-EB tag-human m2 mAChR, flag tag-human beta2 adrenergic receptor-EE tag, human neurokinin 3 receptor-HSV tag-Myc tag, flag tag-human m1 mAChR-EB tag, and rat m3 mAChR-HSV tag-OctaHis tag. The ligand identified by the method of the invention is useful for the development of novel medicines and medicinal diagnostics. The present sequence represents the hydrophobic protein mellitin tag tag-Human beta2-adrenergic receptor EE used in the method of the invention.
Signal sequence; ligand identification, hydrophobic protein; transmembrane protein; monotopic membrane protein; polytopic membrane protein; pump; channel; receptor kinase;
                                                                                                                                              ABG31300
                                                                                                                                                                                ABG31300 standard; Protein; 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     molecule, separating the complex from the unbound molecules, and identifying the ligand molecule. The method of the invention is useful for identifying a ligand for hydrophobic protein such as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention relates to a novel method for identifying a ligand for hydrophobic protein. The method comprises selecting a ligand molecule affinity selection by exposing a hydrophobic target protein bound by a amphiphile to a multiplicity of molecules to promote formation of at least a complex between the hydrophobic target protein and the ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying ligand for hydrophobic protein based on affinity selection which can operate in the presence of amphiphile without regard to the specific biological function of hydrophobic target protein -
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                                                                        Hydrophobic
                                                                                                           21-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 2; 97pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                            LFARGSIVGNMSRFVFDFKADYGGVGENLYVHADDVEFVPGESLKWNVRNLDVMPIFETL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                    MKFLVNVALVFMVVYISYIYARLPDGITKAGEDALRPWKSTAKHPWFQIEDNRCYIDNGK 60
                                                                                                                                                                                                                                                                      IVLAIVFĠNVLVITAIAKFERLQTVTNY
                                                                                                                                                                                                                                                                                                                                                                                                            MKFLVNVALVFMVVYÏSYIYADYKDDDDKMGQP-------------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         451 AA;
                                                                      protein mellitin-flag @Tag-human ml mAChR-EE.
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                                                                                                         (first
                                                                                                         entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.4%; Score 117.5; DB 2
27.7%; Pred. No. 0.00022;
ive 13; Mismatches 45
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Best Local S
Matches 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or transporter protein, or membrane-associated enzyme, or Myc tag-Et tag-human m2 mAChR, flag tag-human beta2 adrenergic receptor-EE tag, human neurokinin 3 receptor-HSV tag-Myc tag, flag tag-human m1 mAChR-EE tag, and rat m3 mAChR-HSV tag-OctaHis tag. The ligand identified by the method of the invention is useful for the development of novel medicines and medicinal diagnostics. The present sequence represents hydrophobic protein mellitin-flag @Tag-human m1 mAChR-EE used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention relates to a novel method for identifying a ligand for hydrophobic protein. The method comprises selecting a ligand molecule affinity selection by exposing a hydrophobic target protein bound by amphiphile to a multiplicity of molecules to promote formation of at least a complex between the hydrophobic target protein and the ligand molecule, separating the complex from the unbound molecules, and identifying the ligand molecule. The method of the invention is useful for identifying a ligand for hydrophobic protein such as a membrane, pump, channel, receptor kinase, G protein-coupled receptor, or transporter protein or membrane, approached the complex for membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying ligand for hydrophobic protein based on affinity selection which can operate in the presence of amphiphile without regard to the specific biological function of hydrophobic target protein -
                                                                                                                                             Synthetic.
                                                                                                                                                                                                         Human; telomerase reverse transcriptase; hTRT; TRT; diagnosis;
prognosis; cell proliferation; cancer; ageing; ribonucleoprotein.
                                                                                                                                                                                                                                                                                                  Glutathione-S-transferase and hTRT fusion protein 8.
                                                                                                                                                                                                                                                                                                                                                                                                                           AAW47008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW47008 standard; Protein; 1189
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                            Misc-difference
                                                                                                                     Homo
                                                                                                                                                                                                                                                                                                                                                               13-AUG-1998
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                                                                                                                sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MKFLVNVALVFMVVYISYIYADYKDDDDKMNTSAPPAVSPNITVLAP----GKGPW
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milarity 51.8%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                         (first entry)
                       Location/Qualifiers 22..23
"enterokinase cleavage site"
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Pred. No. 0.0018;
0; Mismatches 1
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                                                                                                                                                                                                                                                                                                               of the present invention which describes human telomerase reverse transcriptase (hTRT). The present invention also describes the following methods: (A) determining whether a test compound is a modulator of hTRT, by detecting the change in hTRT recombinant transcription of the compound;

(C) a modulator of hTRT, by detecting the change in hTRT recombinant transcription of the compound;

(B) preparation of recombinant telomerase by contacting a protein preparation of hTRT with a telomerase RNA component; (C) detection of the hTRT RNA or protein in a sample by binding a relevant probe to the sample and detecting the complex formed or in the case of the hTRT and the product with presence of hTRT in the sample; and (D) increasing the product with presence of hTRT in the sample; and (D) increasing the proliferation of a vertebrate cell by increasing the expression; and (E) the use of an agent that causes an increase in cell vertebrate cell proliferation to create a medicament that inhibits ageing. A protein preparation of hTRT and the polynucleotide encoding hTRT can be used in the manufacture of medicaments for inhibiting the effect of ageing or cancer. Inhibitors of telomerase activity can be used to treat conditions that are associated with high telomerase.
                                                                                                                                                                                                        Query Match
Best Local 9
                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pure and recombinant human Telomerase Reverse Transcriptase and variants - are useful in the diagnosis, prognosis and treatment cell proliferation conditions especially cancer and ageing
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01-OCT-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GERO-)
(UYTE-)
                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-APR-1997
                                                                                                                                                                                                                                                                                                     activity. A protein preparation of hTRT can also be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-AUG-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present sequence represents a fusion
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                                                                                                                                                                                                        Similarity
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                                                             RAPRCRAVRSLLRSHYREVLPLATEV----RRLGPQGWRLVQRGDPAAFRALVAQCLVCV
                                                                                           EDNRCYIDNGKLEARGSIVGNMSREVEDPKADYGGVGENLYVHADDVEF-----V
                                                                                                                                                          MKFLVNVALVFMVVYISYIYARLPDGITKAG--EDA-----LRPWKSTAKHPWFQI
                           PGESLKWNVRNLDVMPIFETLALRLVLQGDVIWLRC
                                                                                                                             MKFLVNVALVFMVVYISYIYAD-PSSRSAAGTMEFAAASTQRCVLLRTWEALAPATPAMP
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                                                                                                                                                                                                                                                         1189 AA;
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                                                                                                                                                                                          Conservative
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97US-0844419.
97US-0846017.
97US-0851843.
97US-0854050.
97US-0911312.
WDARPPPAAPSFRQVSCLKELVARVLQRLC
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Harley
                                                                                                                                                                                          10; Mismatches
                                                                                                                                                                                                        Score 109.5; DB Pred. No. 0.0067;
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146
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                                                                                                                                                                                          Indels 31;
                                                                                                                                                                                                                         Length 1189;
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                                                                                                                                                                                                                                              This invention describes a novel vascular endothelial growth factor-X (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has culmerary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and act as an angiogenesis and vascularization concertion in the invention is useful for treating concerting cancer, rheumatoid arthritis, psoriasis and diabetic concertinopathy by inhibiting angiogenic activity or inappropriate vascularization including formation and proliferation of new blood concertion and development of tissues, tissue regeneration and organ concerting medicaments for treating wounds such as dermal ulcers, for preparing medicaments for treating wounds such as dermal ulcers, concerts and tissue sores, venous sores, diabetic ulcers and burns and to promote skin graft growth, tissue repair, proliferation of new blood vessels, tissue regeneration and organ repair by promoting angiogenic activity or vascularization. This sequence represents a human VEGF-X protein which can be expressed in Baculovirus/insect cell systems and which is
                                                                                                                                Query Match
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Matches 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-DEC-1998;
18-MAR-1999;
08-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VEGF-X; vascular endothelial growth factor; human; vulnerary; cytostati antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment; angiogenesis regulator; vascularization regulator; cancer; psoriasis; rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair; tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New vascular endothelial growth factor protein, useful for treating or preventing diseases associated with inappropriate angiogenesis activity such as cancer, rheumatoid arthritis, psoriasis and wounds -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAA71984.
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                                                                                                                                                                                                                                vascularization. This sequence represents a can be expressed in Baculovirus/insect cell described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-442669/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     venous sore; diabetic ulcer; burns; skin graft growth
                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (JANC ) JANSSEN PHARM NV
                                                                                                                                                                                                                               bed in the
36
                            61 LFARGSIVGNMSRFVFDPKADYGGVGE------NLYVHADDVEFVPGESLKWNVR 109
                                                                                                                                                 Similarity
                                                                                                MKFLVNVALVEMVVYISYIYARLPDGITKAGEDALRPWKSTAKHPWFQIEDNRCYIDNGK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sprengel, Xu J;
                                                                                                                                                                                                  354 AA;
                                                                                                                                  Conservative
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99US-0124967.
99US-0164131.
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-SSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHSP---
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                                                                                                                                14;
                                                                                                                                Score 106.5;
Pred. No. 0.00
14; Mismatches
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                                                                                                                                                  .0028;
                                                                                                                                                               DB 21;
                                                                  -DPESHHHHHHESNL----- 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gosiewska
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18-MAR-1999;
08-NOV-1999;
                                                                                                                                                                           vulnerary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and antidiabetic activity and acts as an angiogenesis and vascularization regulator. An antisense molecule of the invention is useful for treating or preventing cancer, rheumatoid arthritis, psoriasis and diabetic retinopathy by inhibiting angiogenic activity or inappropriate vascularization including formation and proliferation of new blood vessels, growth and development of tissues, tissue regeneration and organ and tissue repair in a subject. The products of the invention are useful for preparing medicaments for treating wounds such as dermal ulcers, pressure sores, venous sores, diabetic ulcers and burns and to promote skin graff growth tissues comes, diabetic ulcers and burns and to promote the invention are useful for the sores.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment; angiogenesis regulator; vascularization regulator; cancer; psoriasis; rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair; tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore; venous sore; diabetic ulcer; burns; skin graft growth.
                                                                      Sequence
                                                                                                                  skin graft growth, tissue repair, proliferation of new blood vessels, tissue regeneration and organ repair by promoting angiogenic activity or vascularization. This sequence represents a human VEGF-X protein which can be expressed in E. coli systems and which is described in the method
                                                                                                                                                                                                                                                                                                                                                   This invention describes a novel vascular endothelial growth factor-X (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has
                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                    New vascular endothelial growth factor protein, useful for treating or preventing diseases associated with inappropriate angiogenesis activity such as cancer, rheumatoid arthritis, psoriasis and wounds -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (JANC ) JANSSEN PHARM NV.
                                                                                                                 be expressed in E.
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     44;
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                                                                      354 AA;
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99US-0124967.
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                    11.2%; Score 106.5; DB 24.4%; Pred. No. 0.0028;
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    41;
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Query Match
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Matches 23
                                                                                                                                        The present invention relates to vaccine for prevention and/or prophylaxis of infectious salmon anaemia in fish. The invention provides for nucleic acid sequence encoding viral proteins of infectious salmon anaemia virus (ISAV) as well as the isolated protein. Nucleic acids encoding viral protein is useful for the manufacture of a DNA vaccine for diagnosis, treatment and/or prophylaxis of infectious salmon anaemia in fish, and viral protein can be used for the manufacture of antibodies that are specific for ISAV. The present sequence is infectious salmon anaemia virus 92-M fusion protein.
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N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JAN-2000;
29-FEB-2000;
                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                              Claim 7; Page 39-41; 43pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                    anemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel vaccine for treatment and/or prevention of infectious salmon
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Similarity 23; Conser
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11.0%;
llarity 59.0%;
Conservative
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                                               DB 22;
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밁
                                                                                                                             Query Match
Best Local S
Matches 22
                                                                                                                                                                                                                                                                                                                    membrane, integral membrane, transmembrane, monotopic or polytopic membrane, pump, channel, receptor kinase, G protein-coupled receptor, or transporter protein, or membrane-associated enzyme, or Myc tag-EE tag-human m2 mAChR, flag tag-human beta2 adrenergic receptor-EE tag, human neurokinin 3 receptor-HSV tag-Myc tag, flag tag-human m1 mAChR-EE tag, and rat m3 mAChR-HSV tag-OctaHis tag. The ligand identified by the method of the invention is useful for the development of novel medicines and medicinal diagnostics. The present sequence represents the protein sequence of muscarinic acetylcholine receptor in a baculovirus expression vector used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention relates to a novel method for identifying a ligand for a hydrophobic protein. The method comprises selecting a ligand molecule by affinity selection by exposing a hydrophobic target protein bound by an amphiphile to a multiplicity of molecules to promote formation of at least a complex between the hydrophobic target protein and the ligand molecule, separating the complex from the unbound molecules, and identifying the ligand molecule. The method of the invention is useful for identifying a ligand for hydrophobic protein such as a momentum of integral membrane transmembrane monotonic or nolytonic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transmembrane protein; monotopic membrane protein; polytopic membrane protein; pump; channel; receptor kinase; G protein-coupled receptor; transporter protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying ligand for hydrophobic protein based on affinity selection which can operate in the presence of amphiphile without regard to the specific biological function of hydrophobic target protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
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                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                22; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2
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                                                              MKFLVNVALVFMVVYISYIYARLPD 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 45; 97pp; English.
                                                                                                                                                                                                                                                                 496 AA;
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                                                                                                                           Conservative
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                                                                                                                           Score 104; DB 23
Pred. No. 0.0084;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                             cc to express leech active polypeptides. The active polypeptide has
CC a molecular weight of 7000-17,000 Da (as measured by mass
CC a molecular weight of 7000-17,000 Da (as measured by mass
CC Rhynchobdellida, of genus Placobdella and especially of species
CC Rhynchobdellida, of genus Placobdella and especially of species
CC p. papillifera. The polypeptide inhibits the alternate route of
CC complement activation but has substantially no effect on complement
CC complement factor D and/or C3bBb complex. The active polypeptide is
CC useful for manufacturing a medicament and inhibits one or more steps
CC in the alternate pathway of complement activation. It is useful for
CC treating or preventing conditions, such as haemodialysis and
CC cardio-pulmonary bypass, the presence of in-dwelling catheters and
CC extra-arterial stents, rejection of transplanted organs or tissues,
CC autoimmune diseases including lupus arthritis, rheumatoid arthritis,
CC glomerulonephritis, nephritis, nephropathy, sepsis, injury caused to
CC tissues by reperfusion after an ischaemic period and other conditions
CC associated with activation of complement, including anaphylaxis,
CC anemia involving activation of alternate complement pathway in a
CC carfiner
                                                                                                                                Matches
                                                                                                                                                            Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel polypeptides from the leech Placobdella papillifera which inhibit alternate pathway of complement activation, useful for treating rheumatoid arthritis, sepsis, asthma involving alternate complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 14; 80pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Signal peptide of bee venom melittin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-OCT-2001
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                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents a signal peptide, which may be used to express leech active polypeptides. The active polypeptide has
                                                                                                                                                                                                                                                                                                                            patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BIOD-) BIO-DISCOVERY LTD.
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                                                1 MKFLVNVALVFMVVYISYIYA 21
                                                                                                                                21;
  \mathbf{\mu}
                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                             21
                                                                                                                                Conservative
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                                                                                                                                                                                                                                                             AA;
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                                                                                                                                                               10.8%;
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                                                                                                                                                                  Score 102; pred. No.
  21
                                                                                                                                     Mismatches
                                                                                                                                                                  0.00019
                                                                                                                                                                                                    DB 22;
                                                                                                                                                                                           Length
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RESULT 12
ABG31292
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Best Local
                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                    test sample on UDP-glucose:glycoprotein glucosyltransferase (UGGT) activity. The method comprises exposing an acceptor substrate for UGGT to a labelled donor in the presence of the test sample and UGGT. The method is useful for determining UGGT activity. In particular, the method is useful in glucosyltransferase assay and kinetics measurement for determining UGGT activity. UGGT is a soluble enzyme of the endoplasmic reticulum which catalyses the addition of a glucose residue onto asparagine-linked oligosaccharides, which are present on incorrectly folded glycoproteins. The present sequence is the honeybee melittin signal peptide. This sequence was used in the construction of an expression vector for rat UGGT (see AAF60732 and AAB72436).
Signal sequence; ligand identification; hydrophobic protein; transmembrane protein; monotopic membrane protein; polytopic membrane protein; pump; channel; receptor kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Determining the effect of a test sample on UDP-glucose:glycoprotein glucosyltransferase (UGGT), useful for measuring UGGT activity, comprises exposing an acceptor substrate for UGGT to a labeled donor in the presence of UGGT -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UGGT; UDP-glucose:glycoprotein glucosyltransferase; enzyme; honeybee; melittin signal peptide.
                                                        Heterologous
                                                                                    21-OCT-2002
                                                                                                               ABG31292
                                                                                                                                        ABG31292 standard; Peptide;
                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Fig 8; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Melittin signal peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               present invention relates to a method for determining the effect of
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DB; AAF60733.
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ilarity 100.0%;
Conservative
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                                                        sequence
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Pred. No. 0.00019;
0; Mismatches 0;
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Matches 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    membrane, integral membrane, transmembrane, monotopic or polytopic membrane, pump, channel, receptor kinase, G protein-coupled receptor, or transporter protein, or membrane-associated enzyme, or Myc tag-E tag-human m2 mAChR, flag tag-human beta2 adrenergic receptor-EE tag, human neurokinin 3 receptor-HSV tag-Myc tag, flag tag-human m1 mAChR-EE tag, and rat m3 mAChR-HSV tag-OctaHis tag. The ligand identified by the method of the invention is useful for the development of novel medicines and medicinal diagnostics. The present sequence represents a heterologous signal sequence peptide used in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention relates to a novel method for identifying a ligand for a hydrophobic protein. The method comprises selecting a ligand molecule by affinity selection by exposing a hydrophobic target protein bound by an amphiphile to a multiplicity of molecules to promote formation of at least a complex between the hydrophobic target protein and the ligand molecule, separating the complex from the unbound molecules, and identifying the ligand molecule. The method of the invention is useful for identifying a ligand for hydrophobic protein such as a
                                                                                                  Honeybee; melittin; signal sequence; immunoglobulin; B-cell lymphoma; B-cell mediated pathology; cytostatic; immunosuppressive; dermatological; antiinflammatory; neuroprotective; antidiabetic; antithyroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying ligand for hydrophobic protein based on affinity selection which can operate in the presence of amphiphile without regard to the specific biological function of hydrophobic target protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                 Apis melifica.
                                                                                   autoimmune disease.
                                                                                                                                                                         Honeybee melittin signal sequence
                                                                                                                                                                                                                                                ABB10034;
                                                                                                                                                                                                                                                                                  ABB10034 standard; Protein; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 32; Page 80; 97pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                             h 10.8%; Score 102; DB 23;
Similarity 100.0%; Pred. No. 0.00019;
21; Conservative 0; Mismatches 0;
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WO200213862-A2

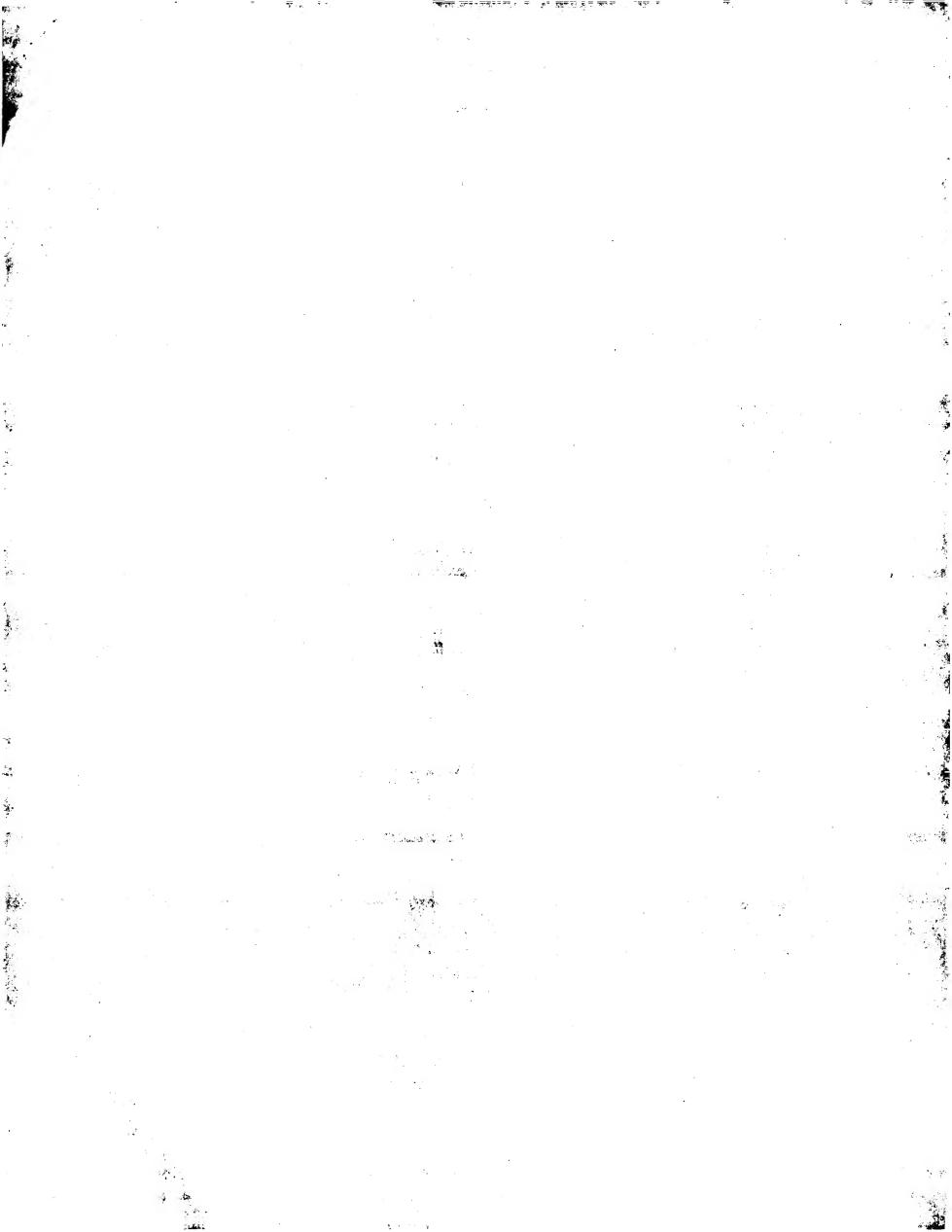
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RESULT 14
AAU76918
ID AAU76
XX
AC AAU76
XX
DT 05-JI
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DE Honey
XX
KW Honey
KW Honey
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OS Apis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence represents the honeybee melittin signal sequence, used in CC the invention to maximise secretion of heterologous proteins from insect cells. The invention relates to a novel composition for altering a B-cell mediated pathology in a patient. The composition contains a chimeric protein comprising at least a portion of a variable region of heavy chain cor light chain (VH or VL) linked to at least a portion of an cimmunoglobulin constant region, where VH or VL region is associated with a B cell clone from the patient having the B cell mediated pathology. The composition of the invention has cytostatic, immunosuppressive, dermatological, antiinflammatory, neuroprotective, antidiabetic, and contithyroid activity. The composition is a vaccine useful for altering a cell mediated pathology. This includes B cell lymphoma e.g.

CC non-Hodgkins lymphoma, refractory low grade or follicular B cell cymphoma; autoimmune disease e.g. multiple sclerosis, systemic lupus erythematosus, anti-Hu associated paraneoplastic neurological syndrome, autoimmune hepatitis, Type I diabetes, autoimmune thyroiditis and cell colony stimulating factor (GM-CSF) or chemokine e.g. monocyte chemotactic colony stimulating factor (GM-CSF) or chemokine e.g. monocyte chemotactic colony stimulating factor (GM-CSF) or chemokine e.g. monocyte chemotactic
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Best Local S
Matches 21
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11-AUG-2000; 2000US-224723P.
23-MAR-2001; 2001US-279079P.
                                                     Honeybee; signal sequence; rheumatoid arthritis; melittin; Vbeta; Valpha; T cell receptor; TCR; cytostatic; neuroprotective; antidiabetic; dermatological; antirheumatic; immunosuppressive; antiinflammatory; antiarthritic; antithyroid; T cell lymphoma; autoimmune disease; multiple sclerosis; systemic lupus erythematosus; diabetes; inflammatory bowel disease; myasthenia gravis; thyroiditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Composition for altering B-cell mediated pathology, has a chimeric protein having portion of variable region of heavy chain or light chail linked to portion constant region associated with patient B cell clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 19; Page 17; 100pp; English
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                    Apis melifica
                                                                                                                                                                                             Honeybee
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                                                                                                                                                                                                                                                                                                             AAU76918 standard; Peptide; 21
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                                                                                                                                                                                             melittin signal sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                MKFLVNVALVFMVVYISYIYA
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RESULT 15
AAM52328
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Best Local
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11-AUG-2000;
01-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Altering T cell mediated pathology in patient, involves administering composition having chimeric protein which has portion of Vbeta/Valpha region of T cell receptor and portion of immunoglobulin constant region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                   Honeybee; signal
                                                                                                                                                                                                                Honeybee melittin signal peptide #1
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21-MAR-2000; 2000JP-0078897.

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                                                                                                                                                                                                                                                                                                     The present invention relates to an expression cassette for executing or promoting the expression of a structural gene. The expression cassette comprises a promoter connected to said structural gene and a secretion signal peptide which is arranged upstream of the structural gene. The present sequence is a signal peptide, which was used in the present
                                                                                                                                                                                                                                                                                                                                                                                                                                            A nucleic acid for promoting the expression of genes, comprises a secretion signal from chicken lysozyme or SF162 type human immunodefficiency syndrome virus -
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N-PSDB; AAI71796.
                                                                                                                                                                                                                                        invention. Note: the present sequence is the SEQ ID 8 as given in the sequence listing. This sequence differs from the SEQ ID 8 given on page 8 (see AAM52506).
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PIR; F26078; QQBEC6.
Early protein; Glycoprotein.
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HQLF1 protein (E glycoprotein).
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STRUCTURE BY NMR OF 44-69.

SPECIES-A.mellifera;

Barnham K.J., Hewish D., Werkmei

Bartone N., Norton R., Rivett D.

Submitted (JUN-1998) to the PDB
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=72098669; PubMed=5139483;
Luebke K., Matthes S., Kloss G.;
"Isolation and structure of N 1-formyl melittin.";
Experientia 27:765-767(1971).
[5]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Apis mellifera (Honeybee), and
Apis cerana (Indian honeybee).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schroeder E., Luebke K., Lehmann M., Beetz I.; "Haemolytic activity and action on the surface tension of solutions of synthetic melittins and their derivatives."; Experientia 27:764-765(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=83287387; PubMed=6309516;
Vlasak R., Unger-Ullmann C., Kreil G.,
"Nucleotide sequence of cloned cDNA co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Apidae; Apis.
NCBI_TaxID=7460, 7461;
                                                                                                                                                    MEDLINE=82189959; PubMed=7076662;
Terwilliger T.C., Eisenberg D.;
"The structure of melittin. II. In
J. Biol. Chem. 257:6016-6022(1982)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SYNTHESIS.
SPECIES=A.mellifera;
                                                                                                                                                                                                                                                   SPECIES=A.mellifera;
                                                                                                                                                                                                                                                                                                                                                                                                    SPECIES=A.cerana;
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                                                                                                                                                                                                                                                                                                                             "Structure of melittin isolated FEBS Lett. 33:241-244(1973).
                                                                                                                                                                                                                                                                                                                                                                                Kreil G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 44-69.
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                                                   Werkmeister J.,
    data bank
                                                                                                                                                                              Interpretation
                                                                                                                                                                                                                                                                                                                                                           from
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                                                        Kirkpatrick A.,
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PIR; A91133; MPHB1.

PDB; 2MLT; 15-JUL-92.

PDB; 1BH1; 06-JAN-99.

InterPro; IPR002116; Melittin.

Pfam; PF01372; Melittin; 1.

ProDom; PD014636; Melittin; 1.
                                                                                                                                                            VESMC
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P59762;
28-FEB-2003 (
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Melittin prec
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Biochim. Biophys. Acta 1031:143-161(1990).
-!- FUNCTION: Main toxin of bee venom with strong hemolytic activity.
Integrates into cell membranes and has multiple effects, probably,
as a result of its interaction with negatively charged
phospholipids. It inhibits well known transport pumps such as the
Na(+)-K(+)-ATPase and the H(+)-K(+)-ATPase. Increases the
permeability of cell membranes to ions, particularly Na+ and
indirectly Ca(2+), because of the Na(+)-Ca(2+)-exchange.
-!- SUBUNIT: Momomer and homotetramer.
-!- SUBCELLULAR LOCATION: Secreted.
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TURN
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REVIEW.
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Dempsey C.E.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE SPECIFICITY: Expressed by the venom gland. MISCELLANEOUS: N-formyl-melittin major has 80% of the activity of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DATABASE: NAME=Protein
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(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
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Pred. No. 0.0022;
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ARTIFACT).
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MELITTIN.
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P06476;
01-JAN-1988
"DNA sequence analysis of the type-common glycoprotein-D herpes simplex virus types 1 and 2.";
DNA 3:23-29(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shi W.J., Zhang S.F., Zhang C.X., Cheng J.A.; "Cloning and sequencing of cDNA coding for prepromelittin hebraeus, Vespa magnifica and Vespula maculifrons."; Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vespula maculifrons (Eastern yellow jacket) (Wasp).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespidae; Vespinae; Vespinae; Vespula.
                                                                                                                                                                  Glycoprotein GD OR US6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch):
                                                                                                                       Herpes simplex virus (type 1 / strain Viruses; dsDNA viruses, no RNA stage; Alphaherpesvirinae; Simplexvirus.
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Shi W.J., Zhang S.F.,
                                                              SEQUENCE FROM N.A. MEDLINE=84131549;
                                                                                                                                                                                               01-JAN-1988
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cytolysis;
SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: Has strong hemolytic activity. Integrates into cell membranes and has multiple effects, probably, as a result of its interaction with negatively charged phospholipids. It inhibits well known transport pumps such as the Na(+)-K(+)-ATPase and the H(+)-K(+)-ATPase. Increases the permeability of cell membranes to ions, particularly Na+ and indirectly Ca(2+), because of the Na(+)-Ca(2+)-exchange (By similarity).

SUBUNIT: Momomer and homotetramer (By similarity).

SUBCELLULAR LOCATION: Secreted (By similarity).

TISSUE SPECIFICITY: Expressed by the venom gland.

SIMILARITY: BELONGS TO THE MELLITIN FAMILY.
                                                                                                          _TaxID=10305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF01372; Melittin; 1.
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06, Last sequence update)
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43
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BY SIMILARITY.
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MELITTIN.
AMIDATION (G-70 PROVIDE AMIDE GROUP) (1 SIMILARITY).
607F52C091C23BB6 CRC64;
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                                                                                                                                       Herpesviridae;
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InterPro; IPR002896; Herpes_glycop_D.

Pfam; PF01537; Herpes_glycop_D.

Glycoprotein; Transmembrane; Signal.

T SIGNAL

1 26 393
FT CHAIN

DOMAIN

26 338
EXTRACELLULAR (POTENTIAL).

FT DOMAIN

26 338
FOTENTIAL.

TDANSMEM

339 363
POTENTIAL.

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26 338
FOTENTIAL.

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27 17.VS-RICH (HIGHLY BASIC
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This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fc entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                        Q69091; O12544; O12833; P03171;
21-JUL-1986 (Rel. 01, Created)
16-OCT-2001 (Rel. 40, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Glycoprotein D precursor.
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                                                                                                                                  McGeoch D.J.;
Submitted (JAN-1989) to the EMBL/GenBank/DDBJ databases.
-!- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1:
                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDLINE=85160822; PubMed=2984429;

McGeoch D.J., Dolan A., Donald S., Rixon F.J.;

"Sequence determination and genetic content of the short unique region in the genome of herpes simplex virus type 1.";

J. Mol. Biol. 181:1-13(1985).
                                                                                                                                                                                                  REVISIONS
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Alphaherpesvirinae; Simplexvirus.
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Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
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SIMILARITY: BELONGS TO THE HERPESVIRUSES GLYCOPROTEIN D FAMILY.
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BELONGS TO THE HERPESVIRUSES GLYCOPROTEIN D FAMILY.
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restrictions on its
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by and for commercial
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Matches 19
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Pfam; PF01537; Herpes glycop_D
Glycoprotein; Transmembrane; S
SIGNAL 25
CHAIN 26 394
DOMAIN 26 339
TRANSMEM 340 364
DOMAIN 365 394
DOMAIN 365 381
PIR; A47627; A47627.

PIR; A47627; A47627.

InterPro; IPR002896; Herpes glycop_D.

Pfam; PF01537; Herpes glycop_D; 1.

Glycoprotein; Transmembrane; Signal.

SIGNAL

CHAIN

26

394

CHAIN

26

DOMAIN

26

394

EXTRACELLULAR (POTENTIAL).

TRANSMEM

340

364

DOMAIN

365

394

CYTOPLASMIC (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

BOMAIN

365

381

ARG/LYS-RICH (HIGHLY BASIC; PROBABLY SERVES TO ANCHOR THE GLYCOPROTEIN IN
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SEQUENCE
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01-JUN-1994
16-OCT-2001
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P36318;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Izumi K.M., Stevens J.G.;
"Molecular and biological characterization of a herpes simplex virus type 1 (HSV-1) neuroinvasiveness gene.";
J. Exp. Med. 172:487-496(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Herpes simplex virus (type 1 / st
Viruses; dsDNA viruses, no RNA st
Alphaherpesvirinae; Simplexvirus.
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GD OR US6.
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GB, GC, GG, GI, AND GE.
-!- SIMILARITY: BELONGS TO THE HERPESVIRUSES GLYCOPROTEIN D FAMILY
                                                                                                                                                                                                                                                                   EMBL; X54361; CAA38245.1; PIR; A47627; A47627.
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MEDLINE=90324869; PubMed=2165127;
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N-LINKED (GLCNAC. ..) (POTENTIAL).

N-LINKED (GLCNAC. ..) (POTENTIAL).

N-LINKED (GLCNAC. ..) (POTENTIAL).

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94B52171P355P6FC CRC64;
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Pred. No.
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ARG/LYS-RICH (HIGHLY BASIC
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stage; Herpesviridae;
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InterPro; IPR002896; Herpes_glycop_D.

Pfam; PF01537; Herpes_glycop_D; 1.

Glycoprotein; Transmembrane; Signal; 3I
SIGNAL 1 25
CHAIN 26 394
DOMAIN 26 339
DOMAIN 26 339
DOMAIN 26 3764
POTENTIAL
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Watson R.J., Weis J.H., Salstrom J.S., Enquist L.W.;
"Herpes simplex virus type-1 glycoprotein D gene: nucleotide sequen and expression in Escherichia coli.";
Science 218:381-384(1982).
-!- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1: GB, GC, GG, GD, GI, AND GE.
-!- SIMILARITY: BELONGS TO THE HERPESVIRUSES GLYCOPROTEIN D FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS7083; P03171;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
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MEDLINE=83016630; PubMed=6289440;
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Herpes simplex virus (type 1 / strain Viruses; dsDNA viruses, no RNA stage;
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ilphaherpesvirinae; Sim
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Pred. No.
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CYTOPLASMIC (POTENTIAL).

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"Cloning and sequencing of cDNA coding for prepromelittin of Polistes hebraeus, Vespa magnifica and Vespula maculifrons.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Main toxin of bee venom with strong hemolytic activity.
Integrates into cell membranes and has multiple effects, probably, as a result of its interaction with negatively charged phospholipids. It inhibits well known transport pumps such as the Na(+)-K(+)-ATPase and the H(+)-K(+)-ATPase. Increases the permeability of cell membranes to ions, particularly Na+ and indirectly Ca(2+), because of the Na(+)-Ca(2+)-exchange (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEL_APICC
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28-FEB-2003 (Rel. 41,
28-FEB-2003 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. SPECIES=A.c.cerana, V.magnifica, and V.v.nigrithorax;
                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                          Cytolysis;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBUNIT: Momomer and homotetramer (By similarity)
-!- SUBCELLULAR LOCATION: Secreted (By similarity).
-!- TISSUE SPECIFICITY: Expressed by the venom gland.
-!- SIMILARITY: BELONGS TO THE MELLITIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Venom gland
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Apidae; Apis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vespa magnifica (Hornet), and Vespa velutina nigrithorax (Hornet).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Apis cerana cerana (Oriental honeybee)
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                                                                                                                                                                                                                                                MOD_RES
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ProDom; PD014636; Melittin; 1.
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                                                                                                                          Similarity
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MKFĹVNVALVFMVVYÍSFÍYAAPEPEPAPEAEAEADAEA
                                                                                               10.4%;
nilarity 59.0%;
Conservative
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Pred. No. 0.00
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AMIDATION (G-70 PROVIDE SIMILARITY).
DA6B17C086C9560C CRC64;
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IT "Cloning and sequencing of cDNA coding for prepromelittin of Polistes

IT "Hebraeus, Vespa magnifica and Vespula maculifrons.";

IL Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.

IL Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.

IT "FUNCTION: Has strong hemolytic activity. Integrates into cell

membranes and has multiple effects, probably, as a result of its

interaction with negatively charged phospholipids. It inhibits

well known transport pumps such as the Na(+)-K(+)-ATPase and the

H(+)-K(+)-ATPase. Increases the permeability of cell membranes to

inns, particularly Na+ and indirectly Ca(2+), because of the

Na(+)-Ca(2+)-exchange (By similarity).

SUBCELLULAR LOCATION: Secreted (By similarity).

ITISUE SPECIFICITY: Expressed by the venom gland.

ITISUE SPECIFICITY: Expressed by the venom gland.
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28-FEB-2003
28-FEB-2003
                                                                                                                                                             COPI DROME STANDARD; PRT; 1409 AA P04146; Q03728; Q24280; Q24555; Q24585; Q24 01-NOV-1986 (Rel. 03, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEL_POLHE
P59261;
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MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                         Copia protein [Contains: (EC 3.4.23.-)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polistes hebraeus (Paper wasp).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
Vespidae; Polistinae; Polistes.
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Shi W.J., Zhang S.F.,
  Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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MELITTIN.
AMIDATION (G-70 PROVIDE AMIDE GROUP)
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R InterPro; lexv...

R InterPro; lexv...

R Ffam; pF00665; rve; 1.

DR Pfam; pF00098; zf-CCHC; 1.

DR Pfam; pF00098; zf-CCHC; 1.

DR PRONTS; pR00939; C2HCZNFINGER.

DR PROSITE; pS00141; ASP PROTEASE; FALSE_NEG.

DR PROSITE; pS00141; ASP PROTEASE; FALSE_NEG.

PROSITE; pS50158; ZF_CCHC; 1.

KW Transposable element; Hydrolase; Aspartyl protease; ATP-binding; Polyprotein; Alternative splicing; Polymorphism; Zinc-finger.

CHAIN 1 270 COPIA VLP PROTEIN (POTENTIAL).

271 1409 COPIA PROTEASE (POTENTIAL).

CCHC-TYPE.
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EMBL; X02599; CAA26445.1; -.
EMBL; X02600; CAA26446.1; -.
EMBL; X02600; CAA26447.1; -.
EMBL; X02600; CAA26447.1; -.
EMBL; X13719; CAA31997.1; -.
EMBL; X13719; CAA38086.1; -.
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Emori Y., Shiba T., Kanaya S., Inouye S
"The nucleotide sequences of copia and
virus-like particles.";
Nature 315:773-776(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; A03324; UFFFC
MEROPS; A11.001; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                          rlyBase; FBgn0013437; copia\GIP.
InterPro; IPR001969; Aspprotease_site.
InterPro; IPR001584; Rve.
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MEDLINE=90151630; PubMed=1689241;
" "Armma H., Zushi M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Miller K., Rosenbaum J.,
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MEDLINE=85267679; PubMed=2410772;
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NCBI_TaxID=7227;
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nucleotide sequence of Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A03324; OFFFCP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          There are no restrictions ong as its content is in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Togashi S., Miyake
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Best Local
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MUTAGEN
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSV2
VGLD HSV2
STANDARD; PRT; 393 AA
P03172;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                          Terhune S.S., Coleman K.T., Sekulovich R., Burke R.L., Spear P.G., Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
-!- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1 AJ 2: GH, GB, GC, GG, GD, GI, AND GE.
-!- SIMILARITY: BELONGS TO THE HERPESVIRUSES GLYCOPROTEIN D FAMILY.
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                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                          gene."
                                                                                                                                                                                                                                                                                                                                        Lasky L.A., Dowbenko D.J.;
"DNA sequence analysis of the type-common glycoprotein-D herpes simplex virus types 1 and 2.";
DNA 3:23-29(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Herpes simplex virus (type 2).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycoprotein D precursor. GD OR US6.
                                                                                                                                                                                                                            Gene
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                                                                                                                                                                                                                                                                                  MEDLINE=84159516;
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                                                                                                                                                                                                                                                      "DNA sequence of the Herpes simplex virus type 2 glycoprotein
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                                                                                                                                                                                                                                                                                                                                                                                            WEDLINE=84131549; PubMed=6321120;
                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10310;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IYMRLPQGISCNSDNVCKLNKAIYGLKQAARCWFEVFEQALKECEFVN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LALRIVLOGDVIWLRCVPELRVDYTSSAYM-----WNMQ
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                                                                                                                                                                                                                                                                                  PubMed=6323270;
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Missing (in isoform Short).

/FTId=VSP 005226.

STTGYLFKMFDFNLICWNTKRQNS -> VQQGIYSKCLILI
SFVGIQRDRTQ (IN VARIANT COPIA-RELATED).

MISSING (IN VARIANT COPIA-RELATED).

D->A: LOSS OF ACTIVITY.

S -> N (IN REF. 2; CAA26447).

I -> V (IN REF. 2; CAA26447).

Q -> E (IN REF. 2; CAA26447).

Q -> E (IN REF. 2; CAA26447).
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Pred. No. 0
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                                                                      collaboration
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RESULT 13
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Best Local S
Matches 17
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MEDLINE=85210904; PubMed=3889347;
MEDLINE=85210904; PubMed=3889347;
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P13778;
01-JAN-1990
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CARBOHYD
CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
DOMAIN
           PIR; S28;
Plasmid;
                                                         This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF01537; Herpes glycop D; 1.
Glycoprotein; Transmembrane; Signal.
SIGNAL 1 25 POTENTIAL.
CHAIN 26 393 GLYCOPROTEIN D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U12180; AAB60552.1; -.
EMBL; U12182; AAB60554.1; -.
EMBL; U12183; AAB60555.1; -.
EMBL; K02373; AAA45842.1; -.
EMBL; K01408; AAA45841.1; -.
                                                                                                                                                                                                                                                                                                      Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Zygosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANT
VARIANT
                                    EMBL; X02398; CAA26244.1; -.
                                                                                                                                                                    "Molecular and functional organization of yeast plasmid pSR1.";
J. Mol. Biol. 182:191-203(1985).
-!- FUNCTION: PLASMID PARTITION REQUIRE REP1, REP2, AND A CIS-ACTING DNA SEQUENCE (KNOWN AS STB). REP 1 MAY ACT BY INTERCALATING IN THE YEAST NUCLEAR MATRIX AND BINDING STB EITHER DIRECTLY OR VIA
                                                                                                                                                                                                                               Muta T., Oshima Y.;
                                                                                                                                                                                                                                                                                        NCBI_TaxID=4956;
                                                                                                                                                                                                                                                                                                                            Zygosaccharomyces rouxii (Candida Plasmid pSR1.
                                                                                                                                                                                                                                                                                                                                                                             01-JAN-1990
01-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF021342; AAB72102.1; -
                                                                                                                                                                                                                                                                                                                                                                  Trans-acting
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002896; Herpes_glycop_D.
                         S28354; S28354.
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17; Conserv
 Trans-acting factor.
410 AA; 46578 MW;
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410 AA;
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Last annotation updat
(REP1).
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Pred. No. 0.19
0; Mismatches
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A -> S (IN STRAINS 333 AND BBKC).

RSV -> AQM (IN STRAINS 333 AND BBKC).

A85148210677777
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N-LINKED (GLCNAC. ..)
N-LINKED (GLCNAC. ..)
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  C9B28C381331F018 CRC64;
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                                                                                                                      a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BBKC)
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Query Match

Score 81;

DB

Length 410;

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RA Schmid G., Englbrecht A., Schmid D.;
RT "Cloning and nucleotide sequence of a cyclodextrin glycosyltransferase gene from the alkalophilic Bacillus 1-1.";
RL (In) Huber O., Szejtli J. (eds.);
RL Proceedings of the fourth international symposium on cyclodextrins, pp.71-76, Kluwer Academic Publishers, Dordrecht and Boston (1988).
CC -1- CATALYTIC ACTIVITY: Degrades starch to cyclodextrins by formation of a 1,4-alpha-D-glucosidic bond.
CC -1- COFACTOR: BINDS TWO CALCIUM IONS.
CC -1- SUBUNIT: Monomer.
CC -1- MISCELLANFOVY ---
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CDGT_BACS2
ID CDGT_B
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InterPro; IPR002909; IPT TIG:
Pfam; PF00128; alpha-amylase; 1.
Pfam; PF02806; alpha-amylase_C; 1.
Pfam; PF00686; CBM_20; 1.
Pfam; PF01833; TIG; 1.
PRINTS; PR00110; ALPHAAMYLASE.
ProDom; PD001568; CBD_4; 1.
SMART; SM00642; Aamy; 1.
SMART; SM00632; Aamy_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Cyclomaltodextrin glucanotransferase precursor
                                                                                                                                         InterPro; IPR006589; Alp amyl cat sub.
InterPro; IPR006048; Alpha amyl_C.
InterPro; IPR006047; Alpha amyl_cat.
InterPro; IPR002044; CBD_4.
InterPro; IPR006046; Glyco_hydro_13.
                                                                                                                                                                                                                      HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus sp. (strain 1-1).
Bacteria; Firmicutes; Bacillales; Bacillaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Cyclodextrin-glycosyltransferase)
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                                                                                                                                                                                                                                                                  MISCELLANEOUS: CGTASE MAY CONSIST OF TWO PROTEIN DOMAINS: THE ONE IN THE AMINO-TERMINAL SIDE CLEAVES THE ALPHA-1,4-GLUCOSIDIC BOND IN STARCH, AND THE OTHER IN THE C-TERMINAL SIDE CATALYZES OTHER ACTIVITIES, INCLUDING THE RECONSTITUTION OF AN ALPHA-1,4-GLUCOSIDIC LINKAGE FOR CYCLIZING THE MALITOOLIGOSACCHARIDE PRODUCED.
                                                                                                                                                                                                                                                     KNOWN AS THE ALPHA-AMYLASE FAMILY.
                                                                                                                                                                                                                      S26399; ALBSX1.
; P31797; 1CYG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -- GEMVCNMITNE--TDYGFDEGGGDDDEGSSVEVQNSQSASPGQDQEAQRAPEAPETSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LQGDVIWLRCVPELRVDY------TS$AYMWNMQYGMVGQ---PELAPEDPEDSA 171
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9; Mismatches
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RESULT 15
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Best Local S
Matches 32
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CHAIN
DOMAIN
ACT_SITE
ACT_SITE
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P39371;
              EMBL; U14003; AAA97206.1; ALT_INIT.

EMBL; AE000501; AAC77266.1; ALT_INIT.

EcoGene; EG12562; yjhT.

InterPro; IPR006652; Kelch_rep.

Pfam; PF01344; Kelch; 2.

Hypothetical protein; Kelch repeat; Repeat; Signal; Complete SIGNAL

1 19 POTENTIAL.
                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: Contains
                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic Acids Res. 23:2105-2119(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                "Analysis of the Escherichia coli genome VI: DNA region from 92.8 through 100 minutes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=95334362; PubMed=7610040; Burland V.D., Plunkett G. III, So
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical pyJHT OR B4310.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Blattner F.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VCBI_TaxID=562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 31, Created)
(Rel. 39, Last sequence update)
(Rel. 42, Last annotation update)
protein yjhT precursor.
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224
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78663
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                                                                                                                                                                                                                                                                                                                                                                                           Contains
19
368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                eria; Gammaproteobacteria; Enterobacteriales; Escherichia.
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Pred. No. 4.5;
28; Mismatches
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HYPOTHETICAL PROTEIN YJHT.
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4D973FB21D0D9B0A CRC64;
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                                                                                                                                                                                                                                                                                                          a collaboration - MBL outstation -
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ry 22, 200	ED 169 PD 260	FETLALRLVL ;	DLNEAGKDST	PDGITKAGED : : SEGLTQVFND	***	84 137 173 219 265 336 367 39572 MW;
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		ELRVD' 	DYGGVGENLYVI :: EDYFFI	AKHPWFQIEDNI : SHAPMGMAGH	DB 1; Length 69; Indels	EA204 CRC64;
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